

<https://participant.turningtechnologies.eu/en/join>  
<https://go.epfl.ch/TurningPointPoll>

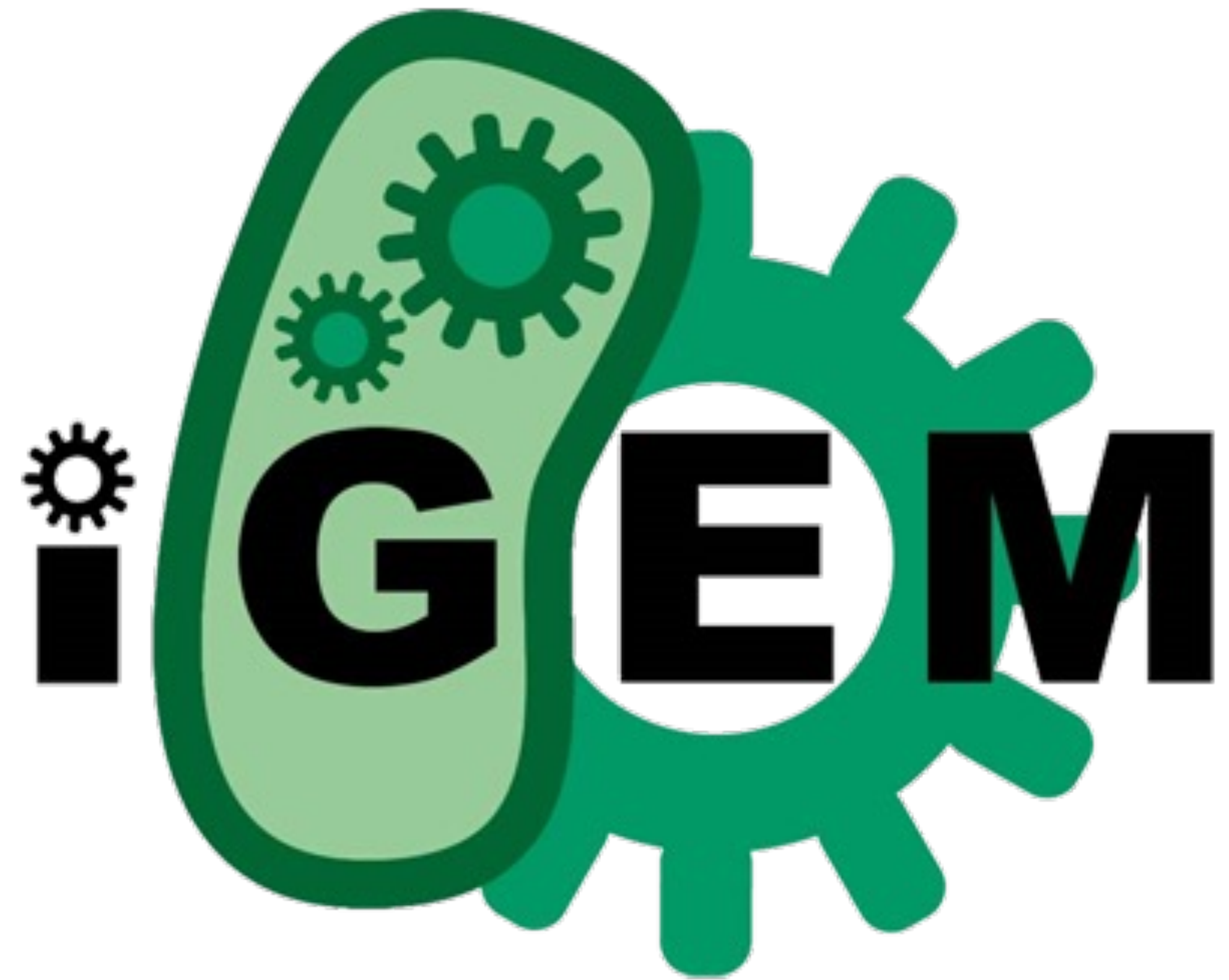
Session ID: **bio411a**



**iGEM**

**Advertisement**

The iGEM Foundation is an independent, non-profit organisation dedicated to the advancement of synthetic biology, education and competition, and the development of an open community and collaboration. This is done by fostering an open, cooperative community and friendly competition.



**Build a Better World with the  
tools of  
Synthetic Biology**

**What synthetic biology experience do you need?**

**None**

# What do students have to do?

**Work as a team** to solve an important problem

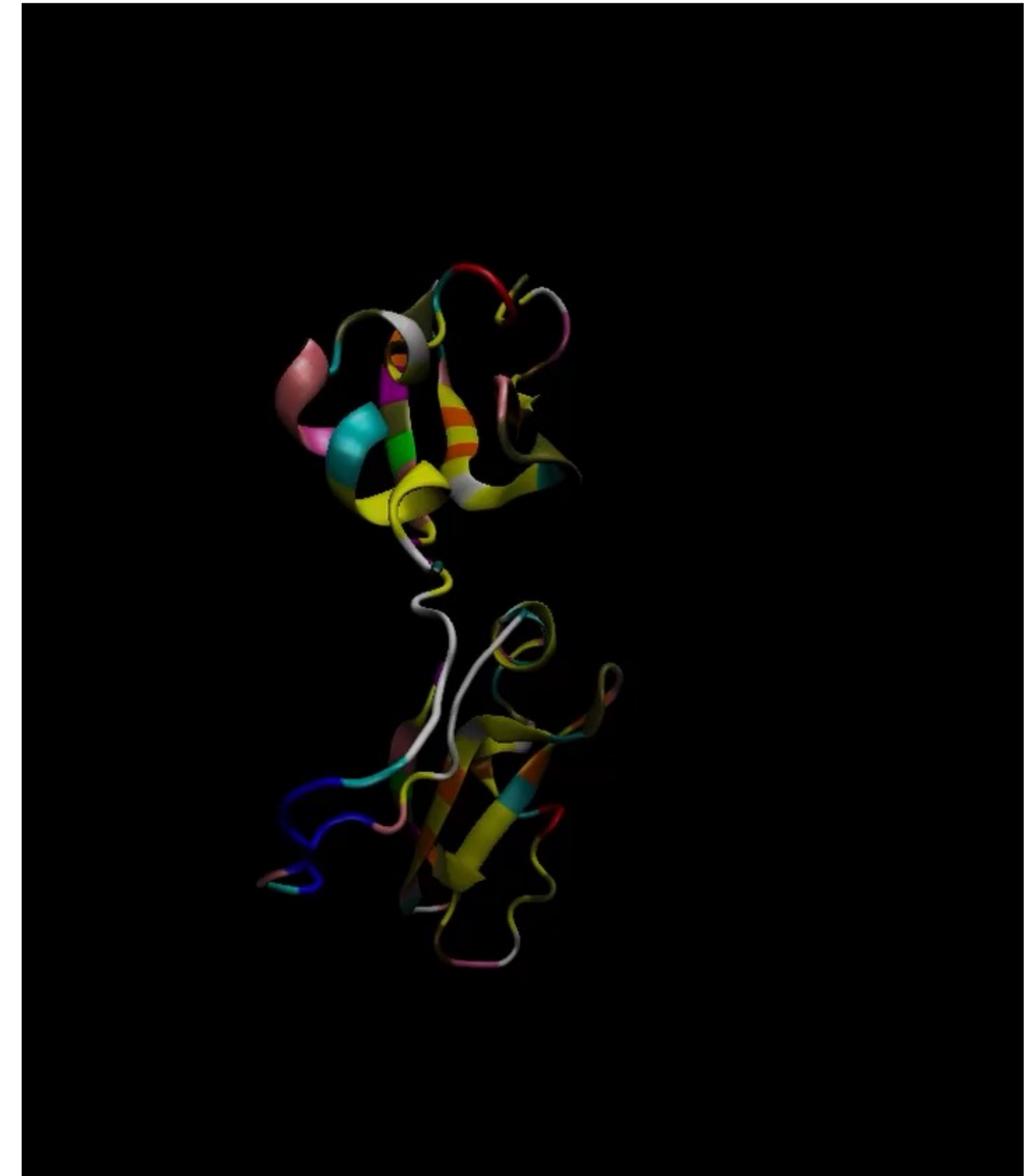
**Work over the summer** (40+ hours a week)

**Represent EPFL** at the iGEM jamboree

12 Credit course

# iGEM project design

- **'Blank Page'** - students decide on topic and approach
- Most often the EPFL topic is related to the **environment or medicine**
- **Interaction** with members of the impacted community is important
- Students **self-organise and vote** on key decisions.



CUP1 LINKER PROTEIN DESIGNED BY 2021 TEAM



# 2026 Team Application

The **2026 iGEM EPFL** team application deadline is  
**12:00 noon CET on the 3<sup>rd</sup> of November 2025.**

<https://go.epfl.ch/igem>



<https://participant.turningtechnologies.eu/en/join>  
<https://go.epfl.ch/TurningPointPoll>

Session ID: **bio411a**

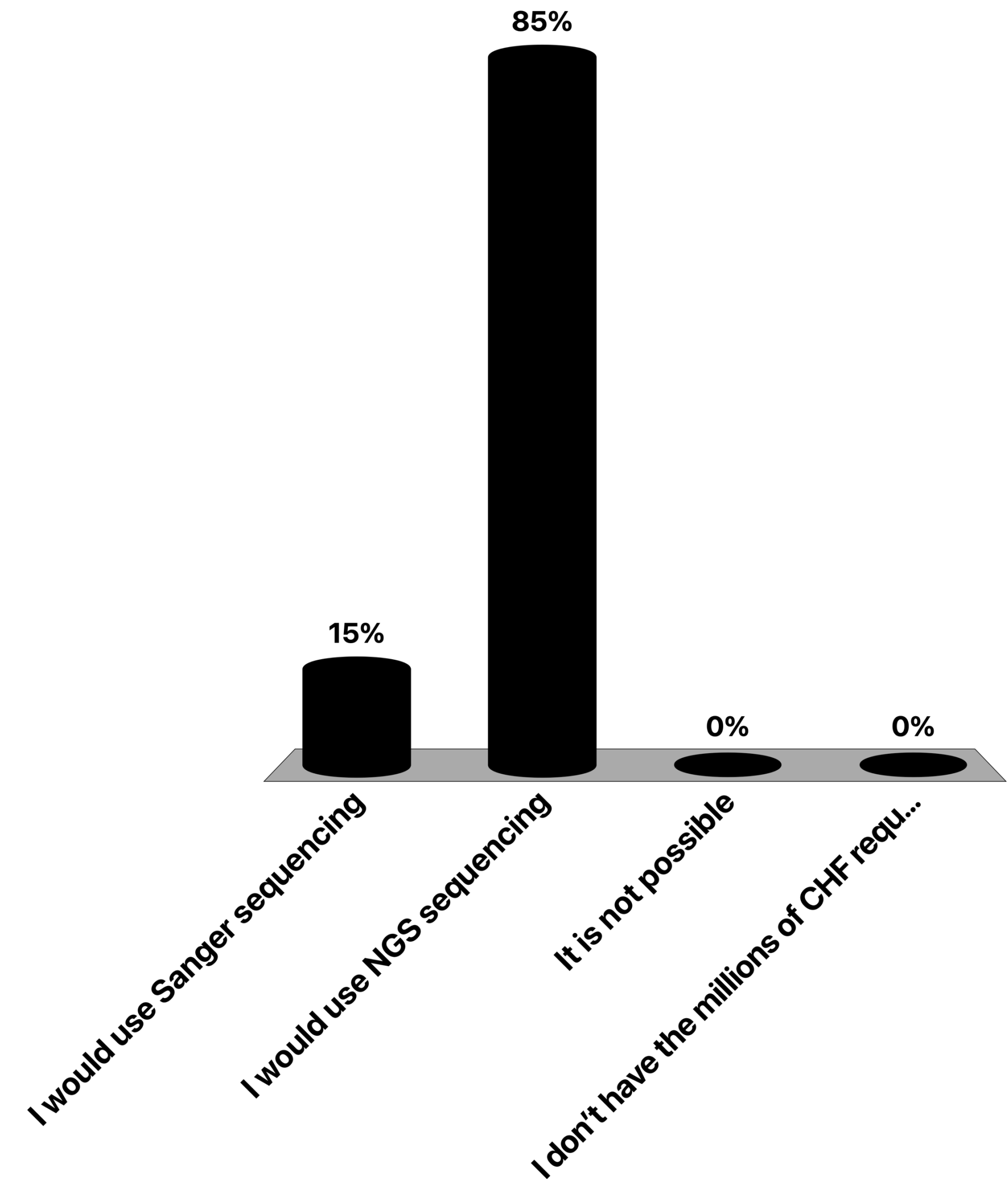




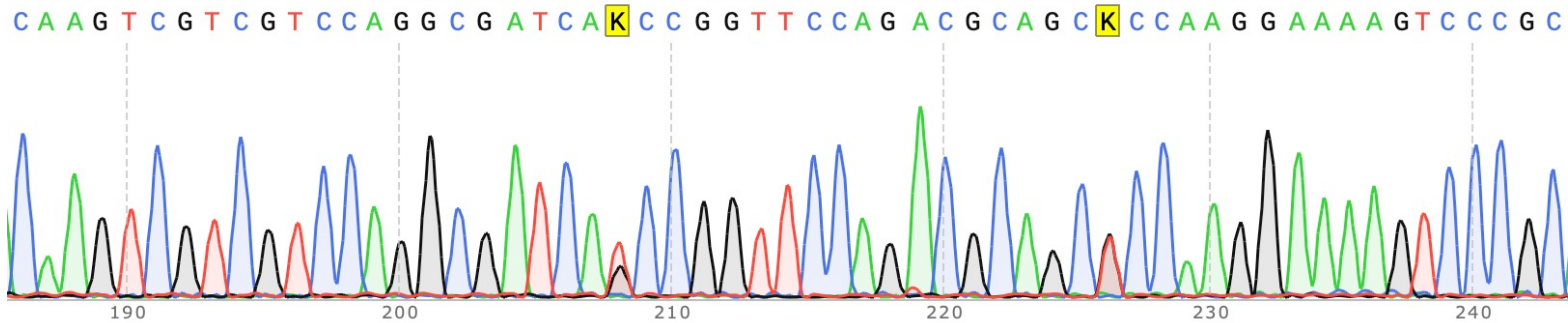
# In Person quiz

# To sequence the genome of the person next to me

- A. I would use Sanger sequencing
- B. I would use NGS sequencing
- C. It is not possible
- D. I don't have the millions of CHF required

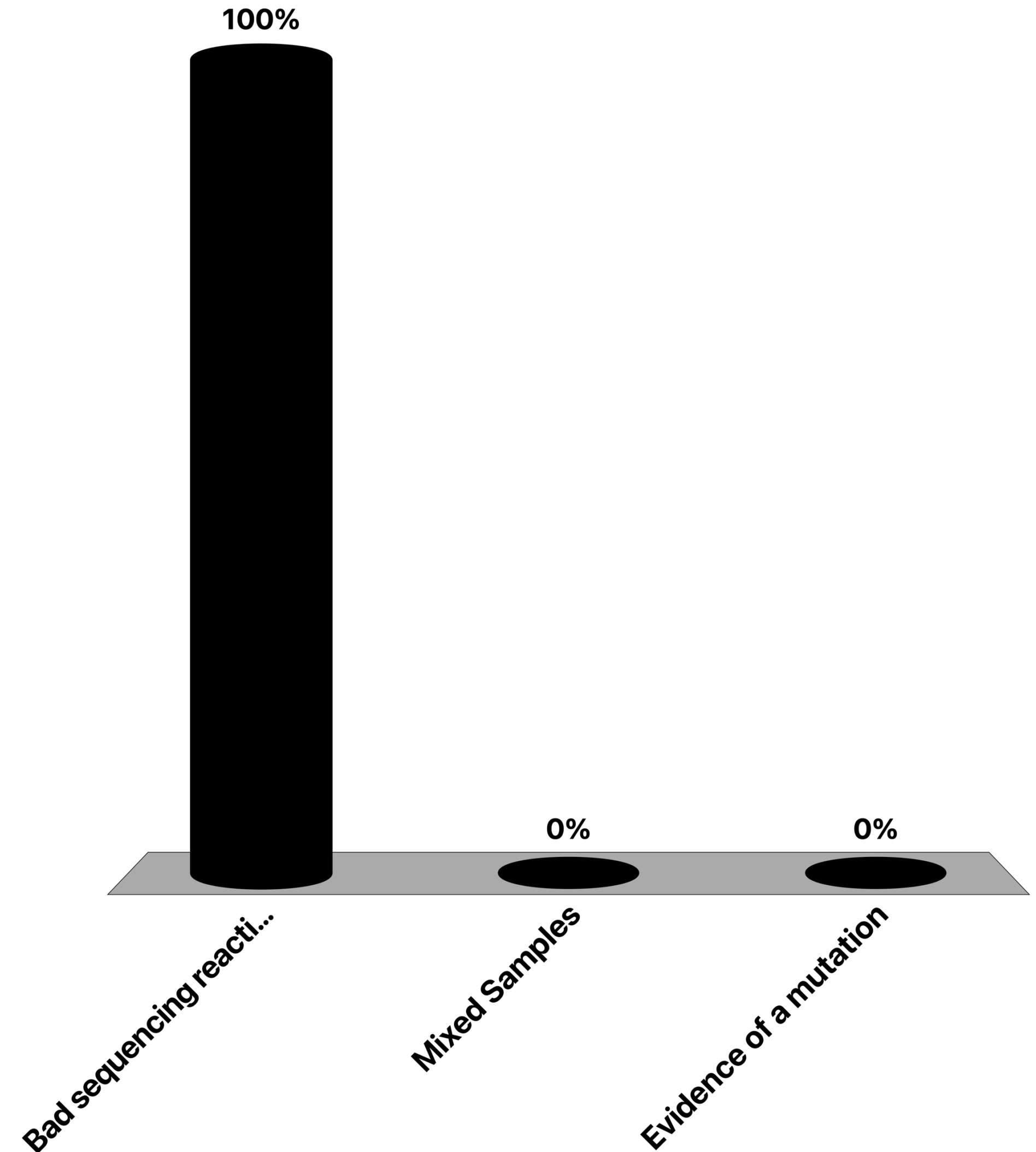


# What is going on here?



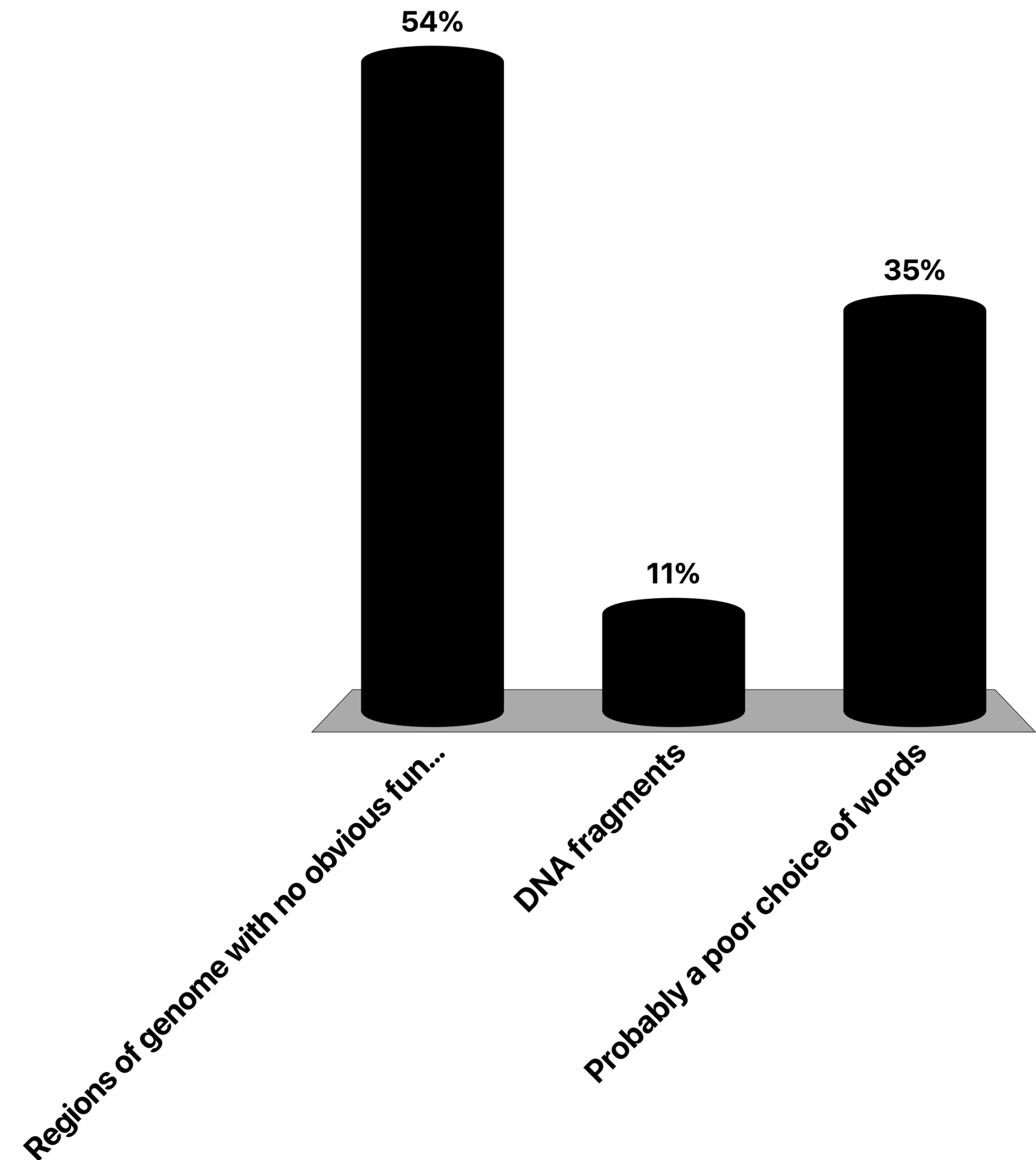
# What is going on here?

- A. Bad sequencing reaction
- B. Mixed Samples
- C. Evidence of a mutation



# Junk DNA is ...

- A. Regions of genome with no obvious function
- B. DNA fragments
- C. Probably a poor choice of words





# Manipulating Nucleotides I

# What is a mutation?

A mutation is an alteration in the genome of an organism

- Chromosomal scale – polyploidy, duplications, inversions, deletions, translocations.
- Nucleotide scale (one or more nucleotides) – insertions, deletions, substitutions.

# Effects on gene products

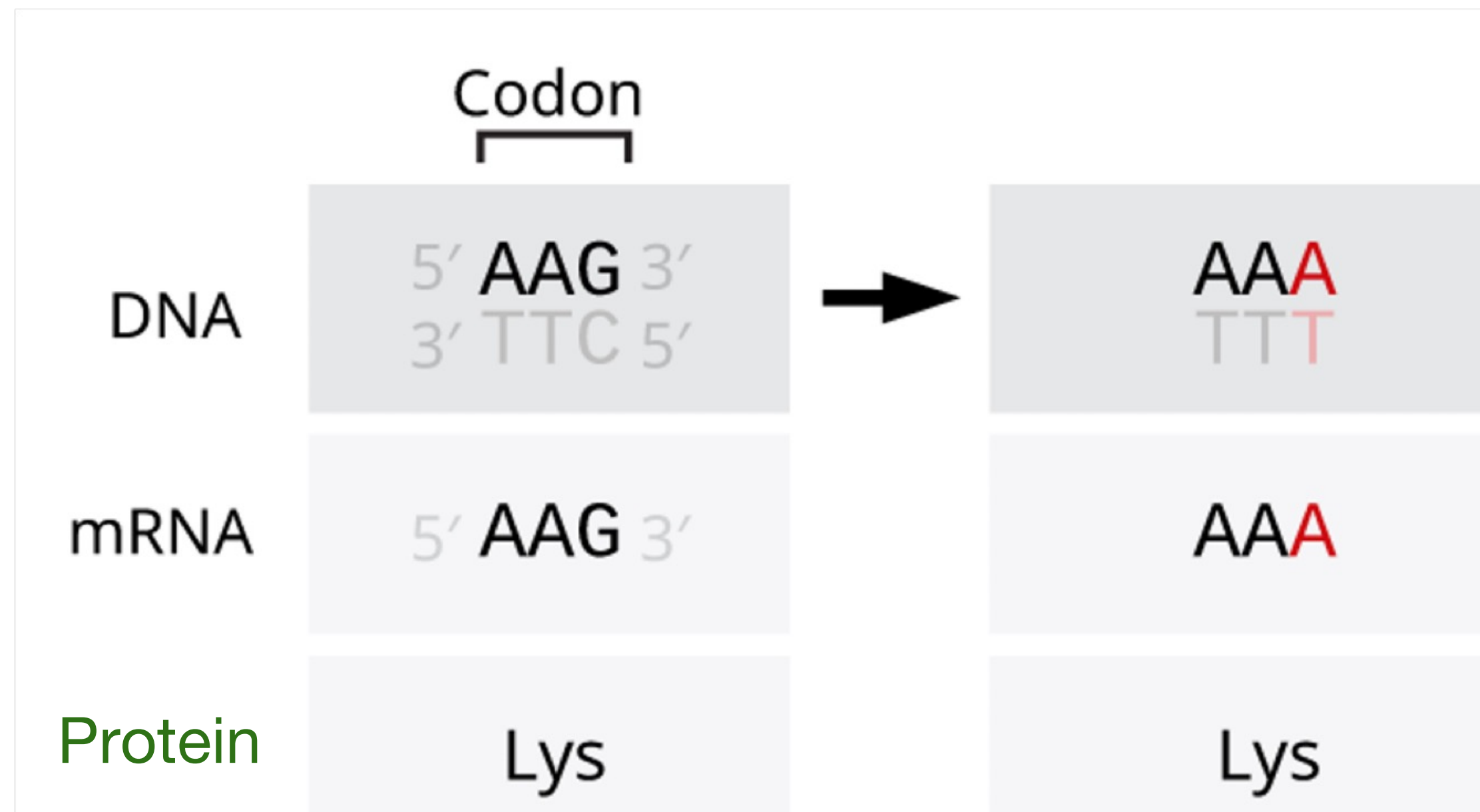
- **Point mutation** – single nucleotide altered
- Effect can be neutral e.g. synonymous substitution

# The Genetic code

		Second letter				
		U	C	A	G	
First letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } <b>UAA Stop</b> <b>UAG Stop</b>	UGU } Cys UGC } <b>UGA Stop</b> UGG Trp	U C A G
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G
	A	AUU } AUC } Ile AUA } <b>AUG Met</b>	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } <b>AAA } Lys</b> <b>AAG }</b>	AGU } Ser AGC } AGA } Arg AGG }	U C A G
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }	U C A G

# Synonymous substitution

‘Silent substitution’



# Codon Usage Bias

Some codons are more favoured than others

- Some specific codons are used more often than other **synonymous** codons during translation of genes
- Can vary **within** a species
- Can vary **between** species.
- Use of 'non-optimal' codons can **reduce** gene expression
- Selection of the optimal codon usage for the host species during **gene synthesis** is a good idea when moving genes between species

Amino acid	Codon	<i>A. thaliana</i>	<i>S. cerevisiae</i>	<i>S. pombe</i>	<i>H. Sapiens</i>
Cys	UGC	+	-	+	+
	UGU	-	+	-	-
Glu	GAA	-	+	-	-
	GAG	+	-	+	+
Phe	UUC	+	+	+	+
	UUU	-	-	-	-
His	CAC	+	+	+	+
	CAU	-	-	-	-
Lys	AAA	-	-	-	-
	AAG	+	+	+	+
Asn	AAC	+	+	+	+
	AAU	-	-	-	-
Gln	CAA	-	-	+	-
	CAG	+	+	-	+
Tyr	UAC	+	+	+	+
	UAU	-	-	-	-

# Effects on gene products

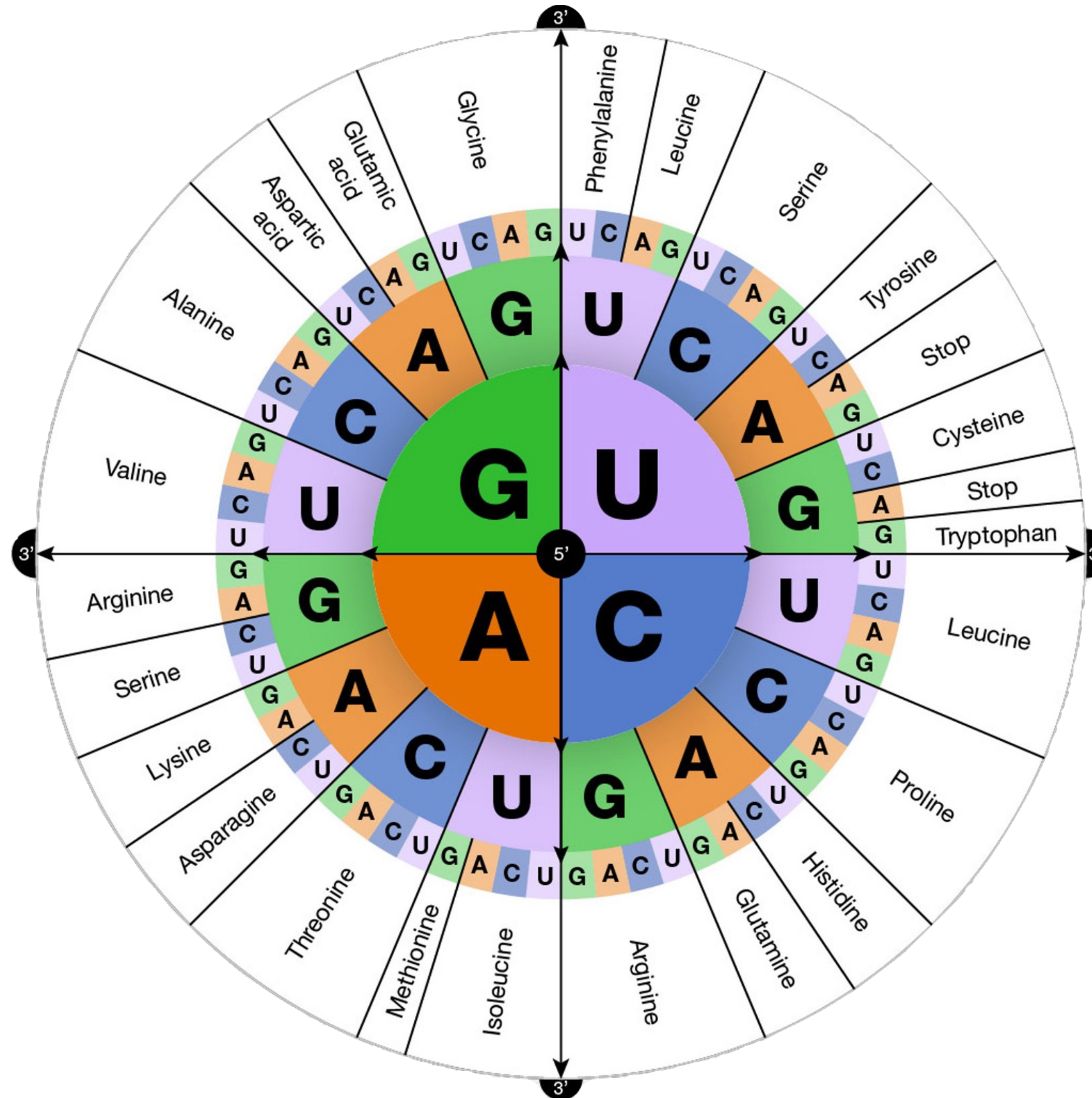
- Point mutation – single nucleotide altered
- Effect can be neutral e.g. synonymous substitution
- Change codon to encode a **different amino acid**.

# Nonsynonymous mutation

Change amino acid



# The Genetic code

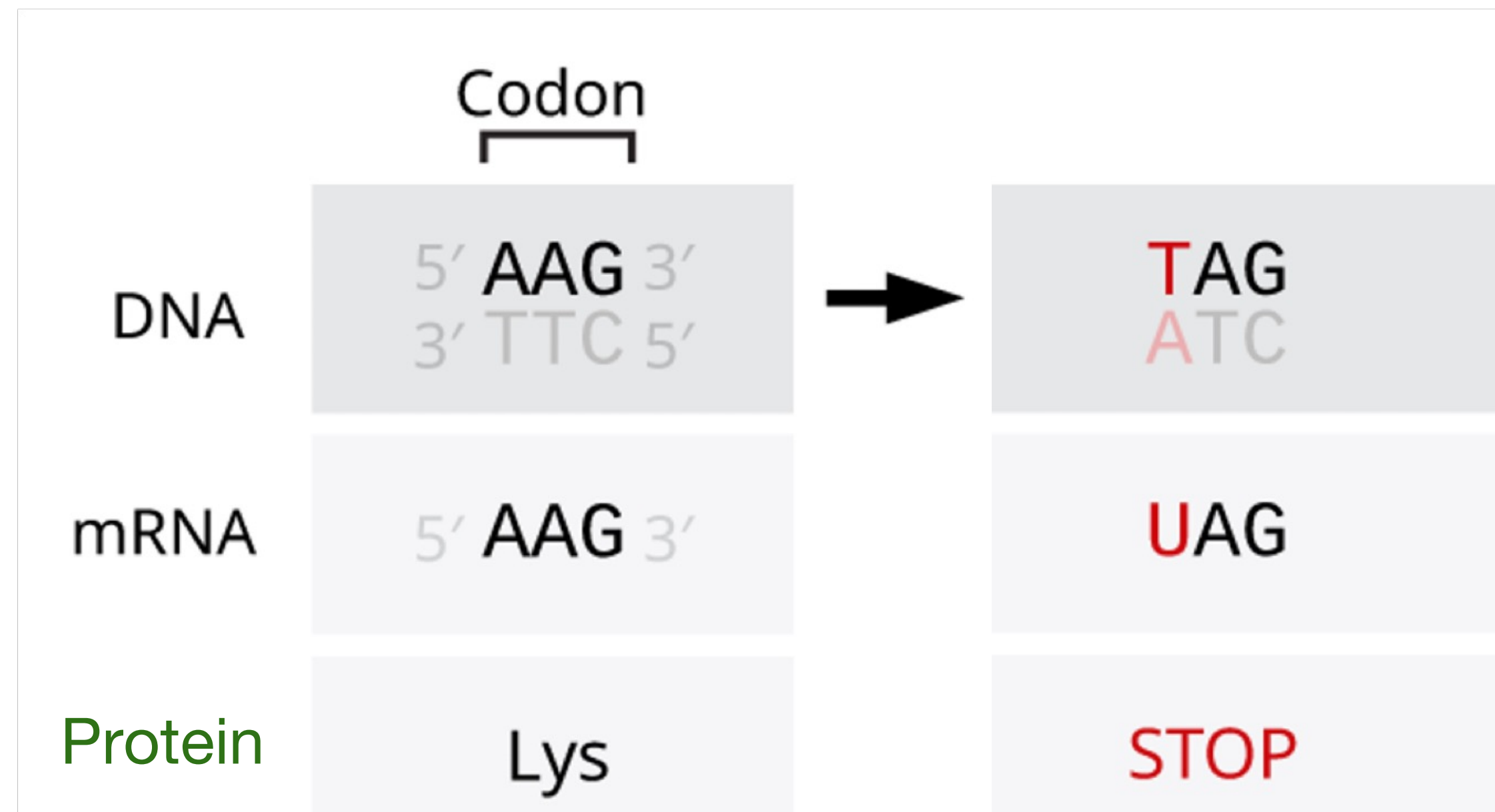


# Effects on gene products

- Point mutation – single nucleotide altered
- Effect can be neutral e.g. synonymous substitution
- Change codon to another amino acid.
- Introduce a **new stop codon** i.e. ‘premature stop’ or ‘nonsense’ mutation

# Synonymous substitution

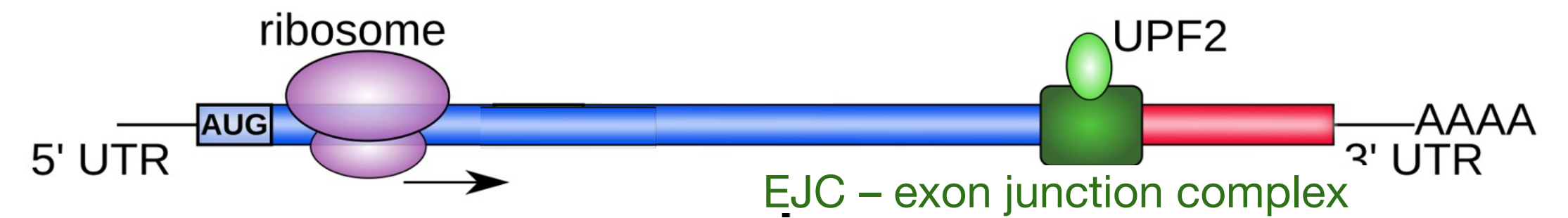
'nonsense mutation'



# Nonsense-mediated decay

## NMD

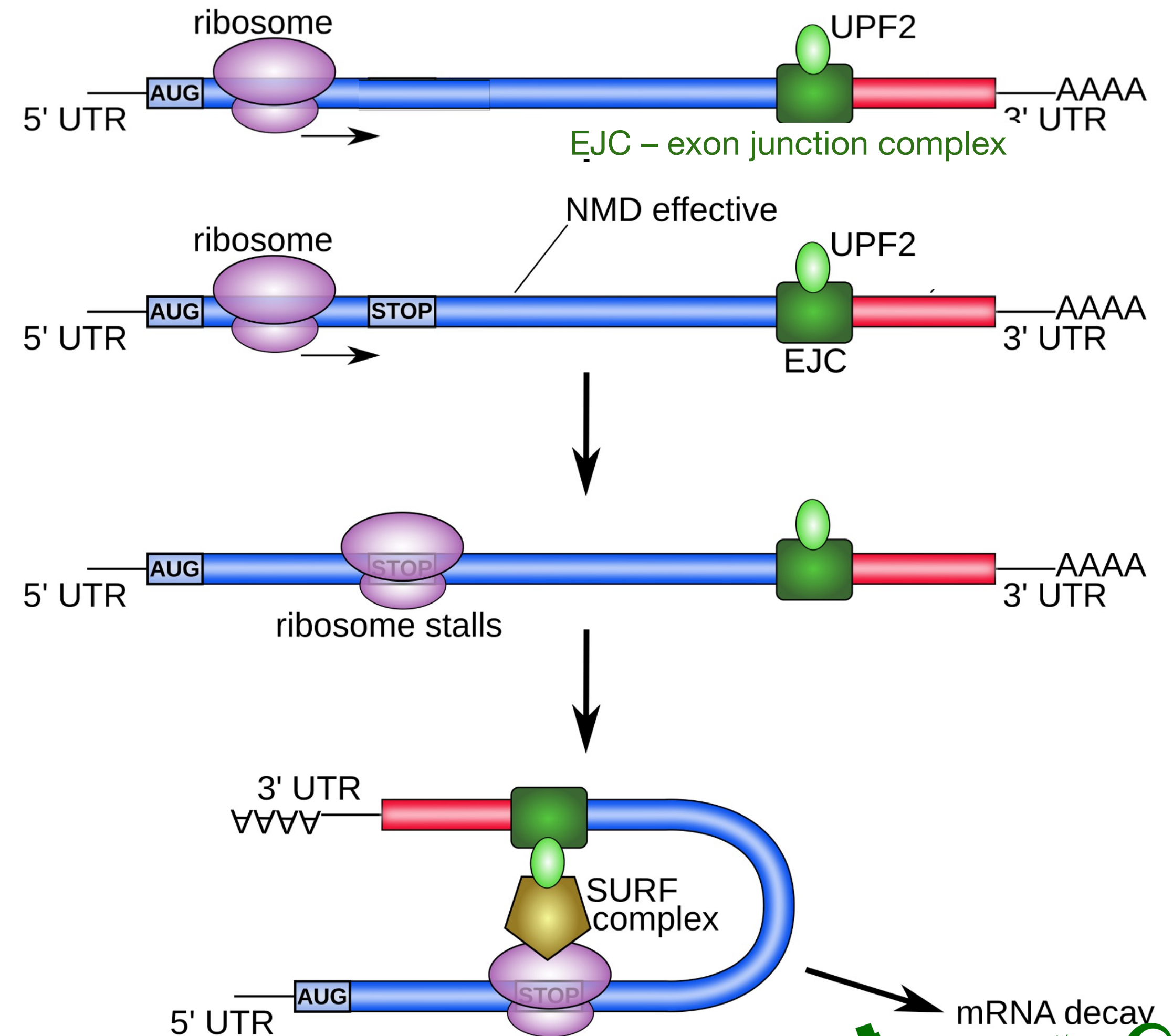
- NMD is a **surveillance mechanism** for errors in gene expression
- **Degrades mRNA transcripts** that contain premature stop codons
- After splicing, exonic-junction complexes (EJCs) remain 20–24 nucleotides upstream of every exon junction and can bind UPF2 proteins.
- If a ribosome encounters a premature stop codon, **it stalls**, allowing a complex with a downstream EJC/UPF2 promoting **mRNA decay** through the SURF complex.



# Nonsense-mediated decay

## NMD

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# Effects on gene products

- Point mutation – single nucleotide altered
- Effect can be neutral e.g. synonymous substitution
- Change codon to a different amino acid.
- Introduce a new stop codon
- **Frameshift** mutation

# Frameshift mutation

- Insertion or deletion of nucleotides that are **not in multiples of 3**
- Changes the reading '**frame**' and thus the protein sequence that will be produced.
- Often results in a premature stop codon.

TAT TGG CTA CTA CAT  
Tyr Trp Leu Val His

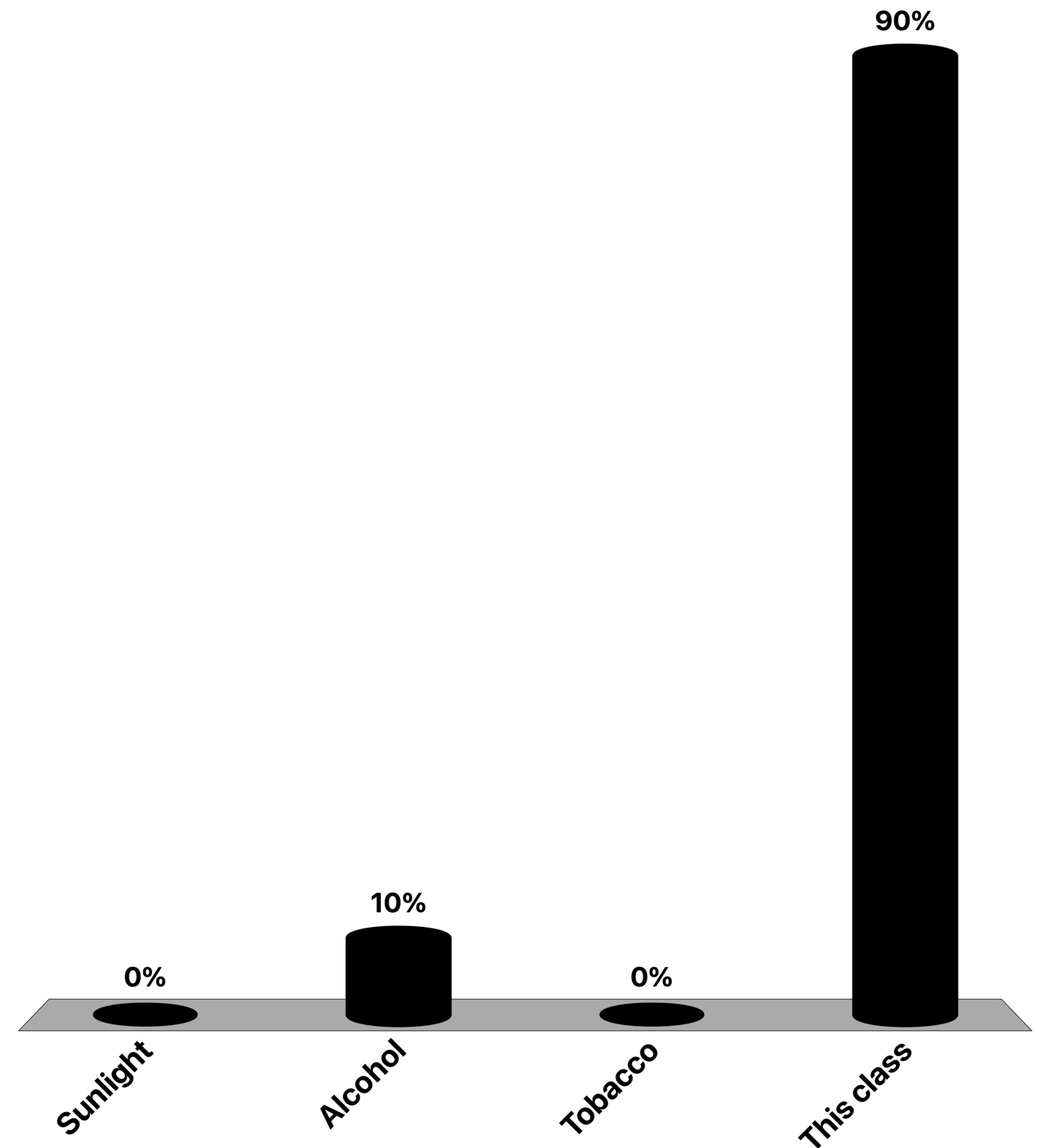
TAT TCG GCT AGT ACA T..  
Tyr **Ser** Ala **Ser** Thr



# In Person quiz

# Which one is not a source of mutation?

- A. Sunlight
- B. Alcohol
- C. Tobacco
- D. This class



# 'Natural' Sources of mutations

## Pass the sunblock

- **Spontaneous** mutations – chemical changes to nucleotides
- **Replication** errors
- **DNA repair** errors
- Environmental **mutagens** – **radiation** e.g. Ultraviolet light, ionising radiation e.g. gamma radiation, **chemicals** that can cause oxidative or other damage.
- Median **somatic** mutation rate per base pair is  $2.8 \times 10^{-7}$  per generation for humans. Order of magnitude **lower in germline cells.**



# Effects of mutations

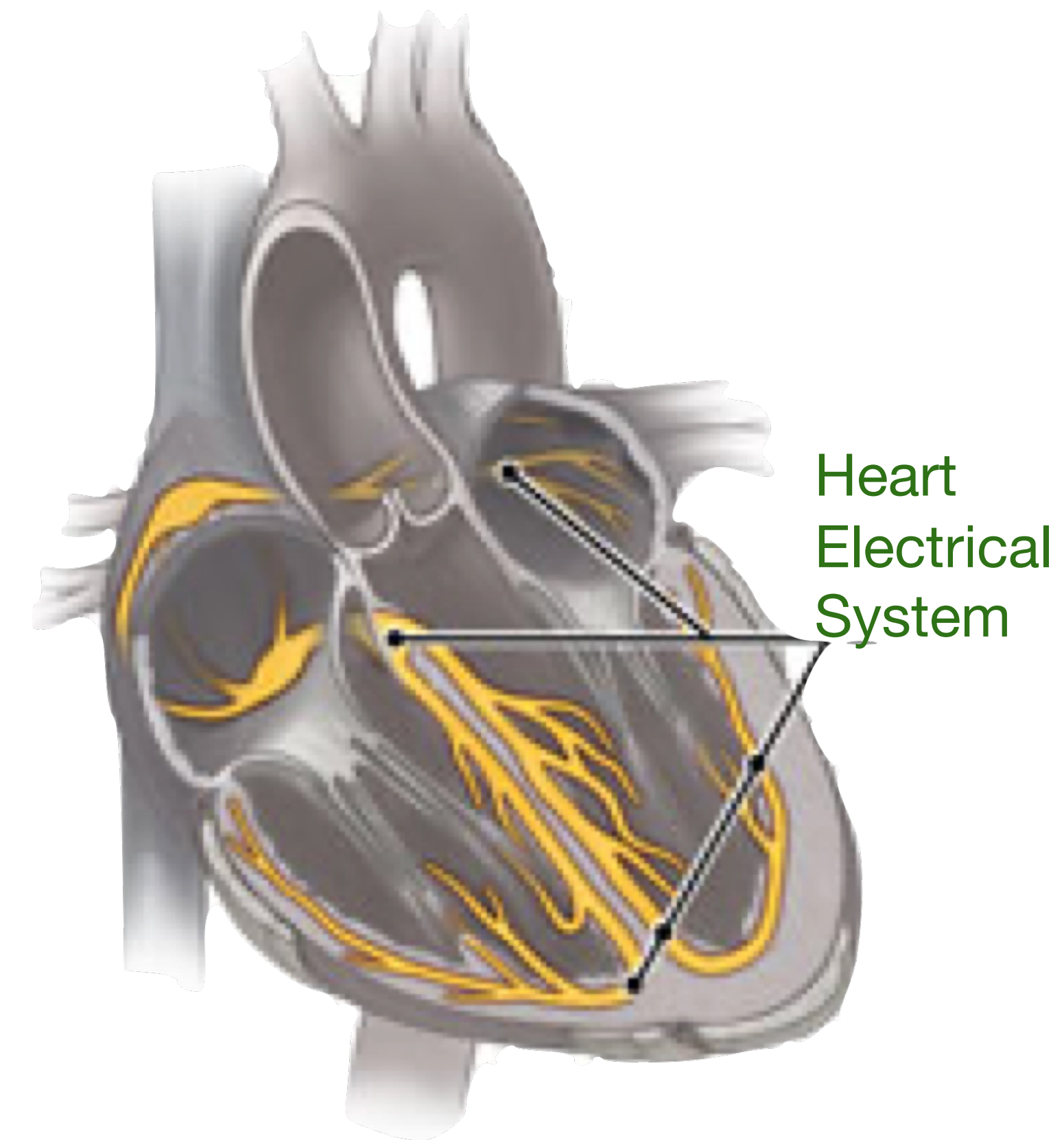
## Not usually superpowers

- **Loss-of-function (LOF)** mutations - gene product function reduced (**partial LOF, hypomorph**) or no function (**null allele, amorph**). If no protein produced at all, called 'protein null'.
- Often **recessive** (i.e. both alleles must to be mutant to observe a phenotype) but can be **haploinsufficient** (loss of one allele can cause a phenotype)
- Human disease examples – **Recessive** e.g. Cystic fibrosis. **Haploinsufficient** e.g. DiGeorge syndrome (22q11 deletion)



# Effects of mutations

- **Gain-of-function (GOF) mutations (hypermorphs).**
- Gene product activity is **increased**. Examples include mutations that increase protein expression or increase protein activity.
- GOF mutations often produce **dominant phenotypes** (i.e. one mutated allele is sufficient to produce a phenotype).
- Related are **Neomorphs** – mutations causing **novel gene product functions** (e.g. expression outside of normal tissues, interaction with novel proteins).
- Human disease example - **Brugada syndrome** (GOF mutants in *KCNE3*) can cause sudden cardiac death in young people



# Effects of mutations

- **Dominant Negative (DN) mutations (antimorphs)** produce altered gene products that act antagonistically to inhibit to the normal gene product.
- Mutations usually have an altered molecular function (commonly reduced activity)
- DN mutations often produce **dominant phenotypes** (i.e. one mutated allele is sufficient to produce a phenotype).
- Human disease example - **Marfan syndrome** (Dominant negative mutants in FBN1), affects connective tissue.



# 2025 Team Application

The **2025 iGEM EPFL** team application deadline is **12:00 noon CET on the 30th of September 2024.**

<https://go.epfl.ch/igem>





# Genetic Model Organisms

# Whistle-stop tour of genetic model organisms

## *Saccharomyces cerevisiae* (Bakers yeast)

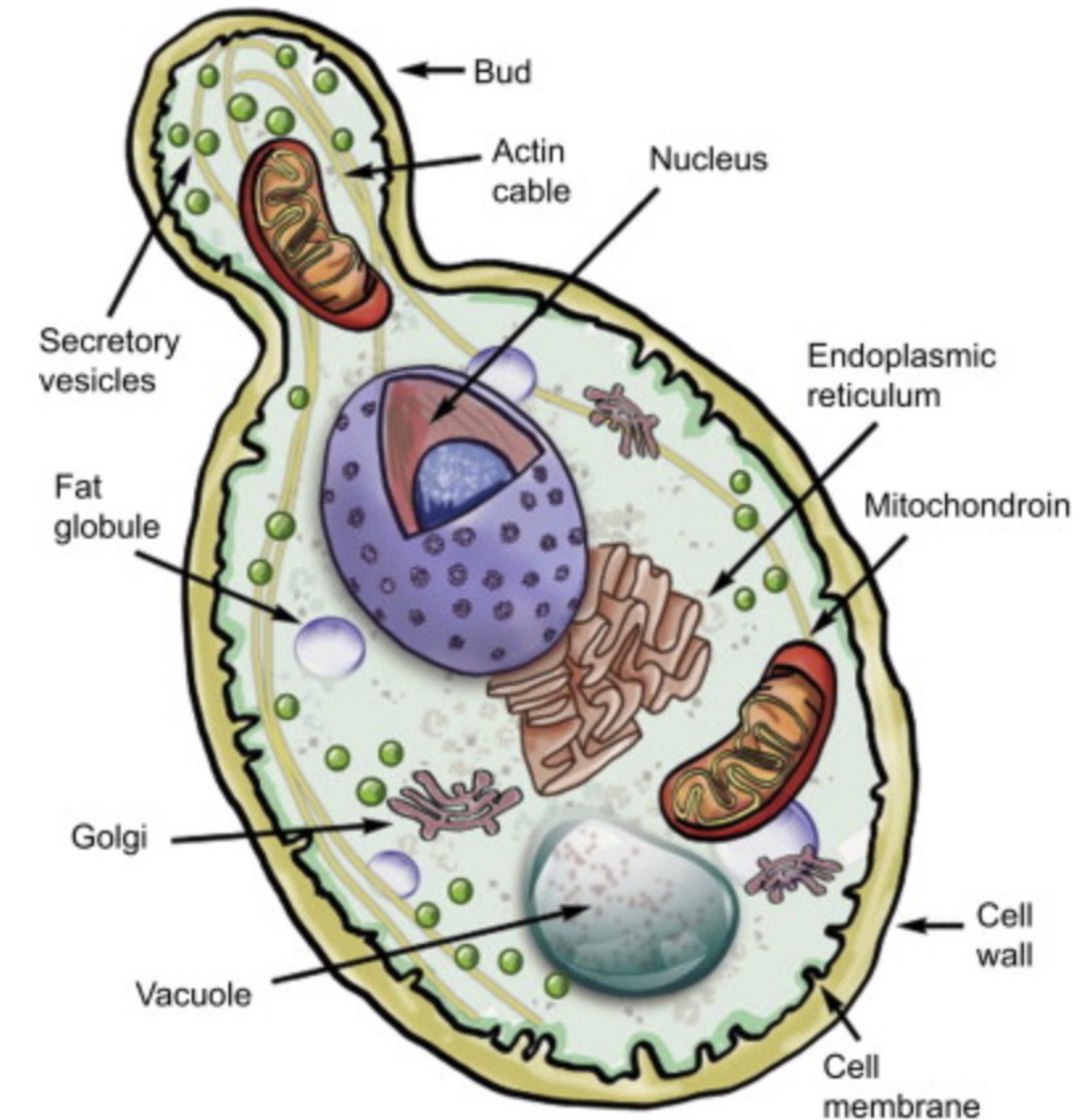
Single cell model organism

Easy to culture, doubling time at 30°C of ~90 minutes

Genome size 12 Mb, 16 chromosomes.

6604 protein coding genes, ~2000 non-coding genes,

Mutants in every gene available



# Whistle-stop tour of genetic model organisms

## *Caenorhabditis elegans* (nematodes)

1000 somatic cells in adults plus  
1000-2,000 germ cells

Generation time 3 days at 25°C

Genome size 100 Mb, 12  
chromosomes

20,470 protein coding genes, ~1300  
non-coding genes, mutants in  
most genes available



# Whistle-stop tour of genetic model organisms

*Drosophila melanogaster* (fruit flies)

>million cells

Generation time 10 days at 25°C

Genome size 180 Mb, 4 chromosomes

13,968 protein coding genes, 4,044 non-coding genes, mutants in most genes available



<https://drosophila.epfl.ch>

# Whistle-stop tour of genetic model organisms

## *Danio rerio* (Zebrafish)

millions of cells

Generation time 3 months

Genome size 1.4 Gb, 25 chromosomes

25,545 protein coding genes, 6,599 non-coding genes, mutants in some genes available



# Whistle-stop tour of genetic model organisms

*Mus Musculus* (mice)

Millions of cells

Generation time 10 weeks

Genome size 2.6 Gb, 20 chromosomes

22,213 protein coding genes, 17,398  
non-coding genes, mutants in some  
genes available



# Whistle-stop tour of genetic model organisms

*Arabidopsis thaliana* (Thale cress)

millions of cells

Generation time 6 weeks

Genome size 1.35 Gb, 5 chromosomes

27,655 protein coding genes, 5,178 non-coding genes, mutants in some genes available

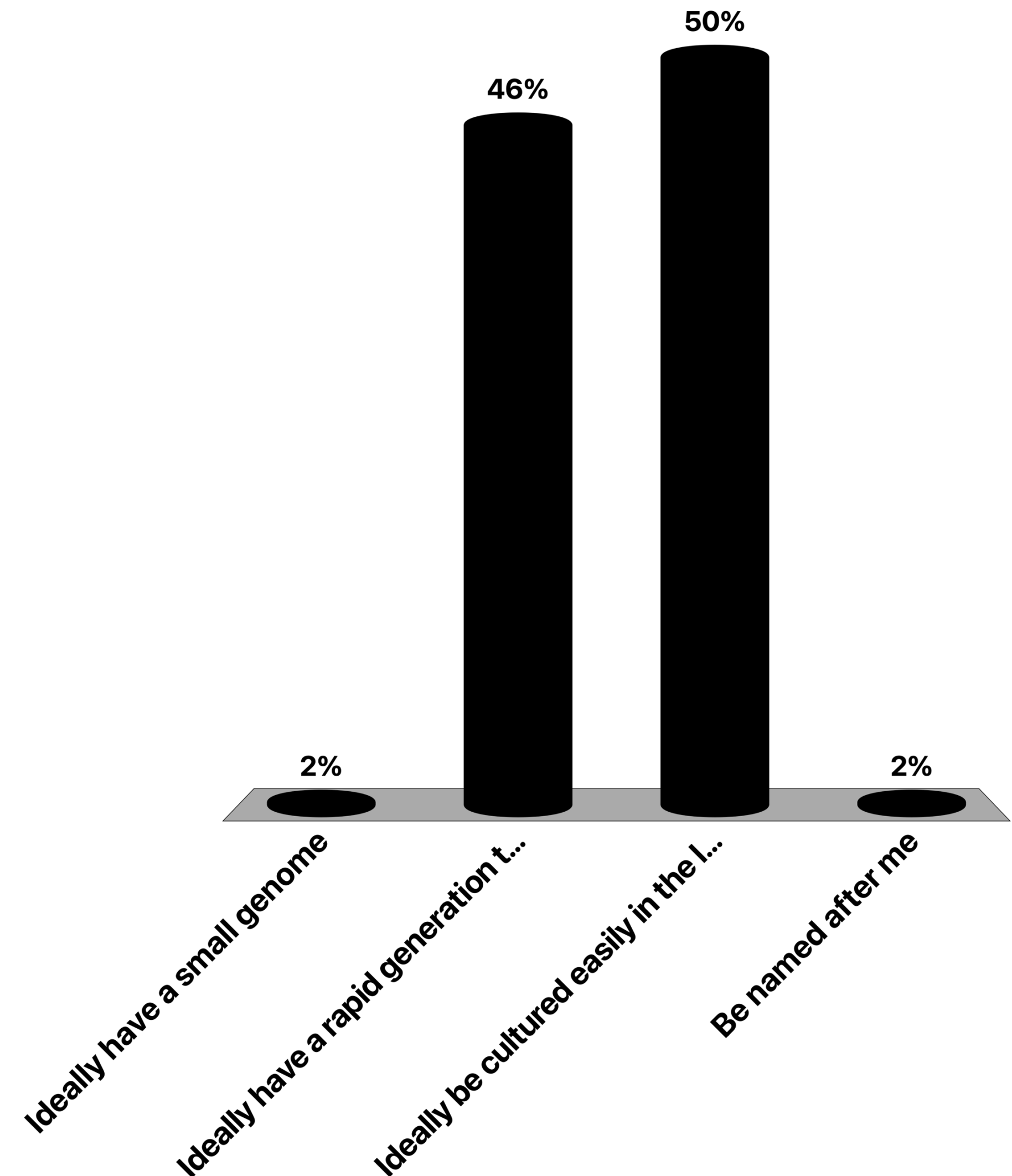




# In Person quiz

# If I was to propose a new model organism it would

- A. Ideally have a small genome
- B. Ideally have a rapid generation time
- C. Ideally be cultured easily in the lab
- D. Be named after me





# Transgenesis

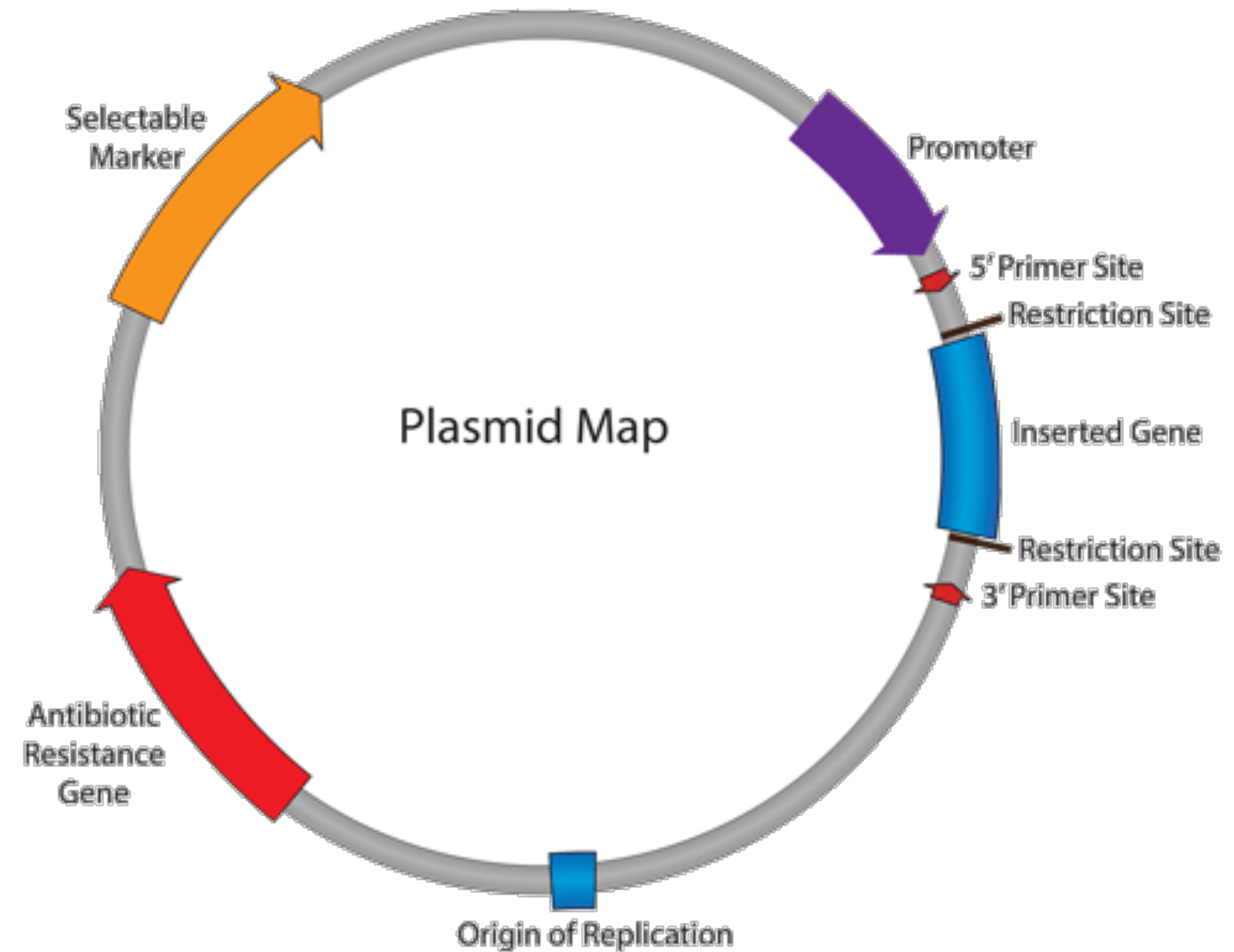
# What is Transgenesis?

- The process of introduction of a transgene into an organism
- A transgene is any exogenous genetic sequence either derived from the same species (e.g. an extra copy of a gene), a different species or an artificial sequence.
- Most transgenic animals are generated for research but transgenic animals (GMO – genetically modified organisms) are used in agriculture.

# Transgene Donor constructs

## Plasmids

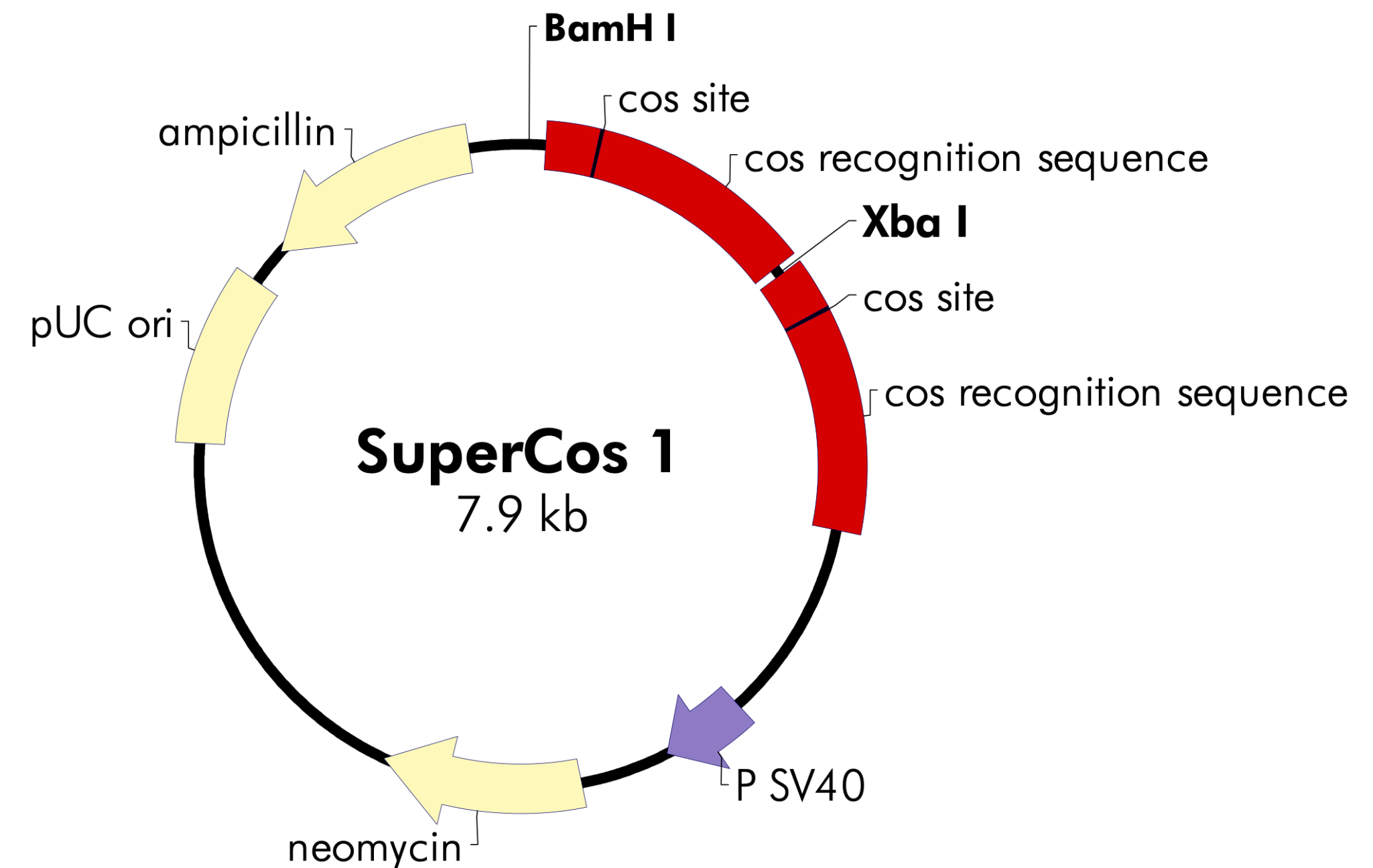
- Easy to work with - Convenient size (generally 1,000-20,000 bp), grow in bacteria (often e.coli).
- Self-replicating - endless number of copies.
- Stable – store in freezer or even dried.
- Useful for lots of things, not species limited, many types of sequences proteins, RNA's etc. etc.
- Larger DNA sequences are difficult.



# Transgene Donor constructs

## Cosmids

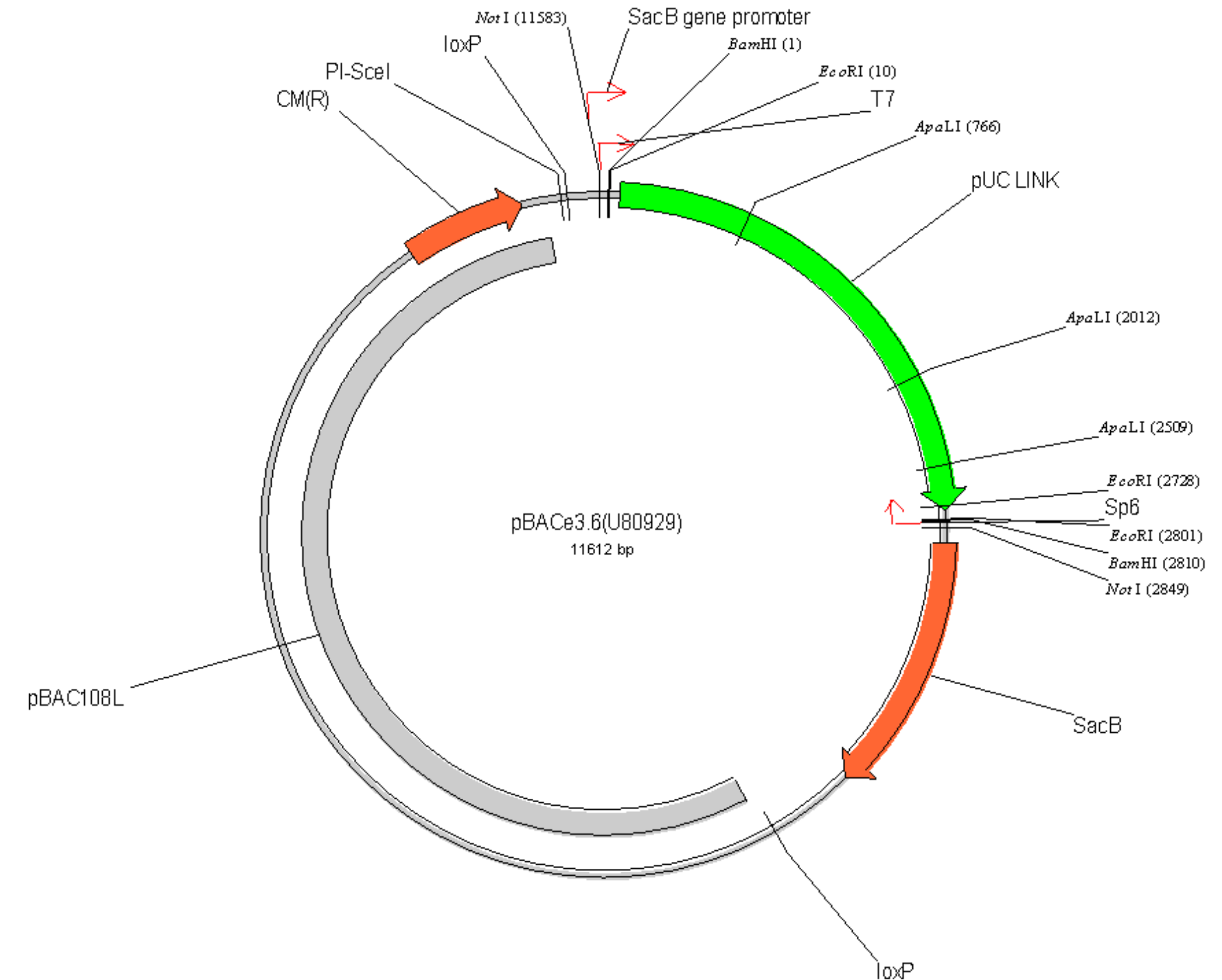
- **Cos** sequence containing plasmid
- Can replicate like a plasmid but unlike plasmids can be packaged in phages.
- Can accommodate larger DNA fragments ranging in size from 30 to 45 kb.
- DNA fragments have to be introduced by restriction digestion.
- Most useful for larger genomic DNA fragments, less so for engineered constructs.



# Transgene Donor constructs

## BACs & YACs

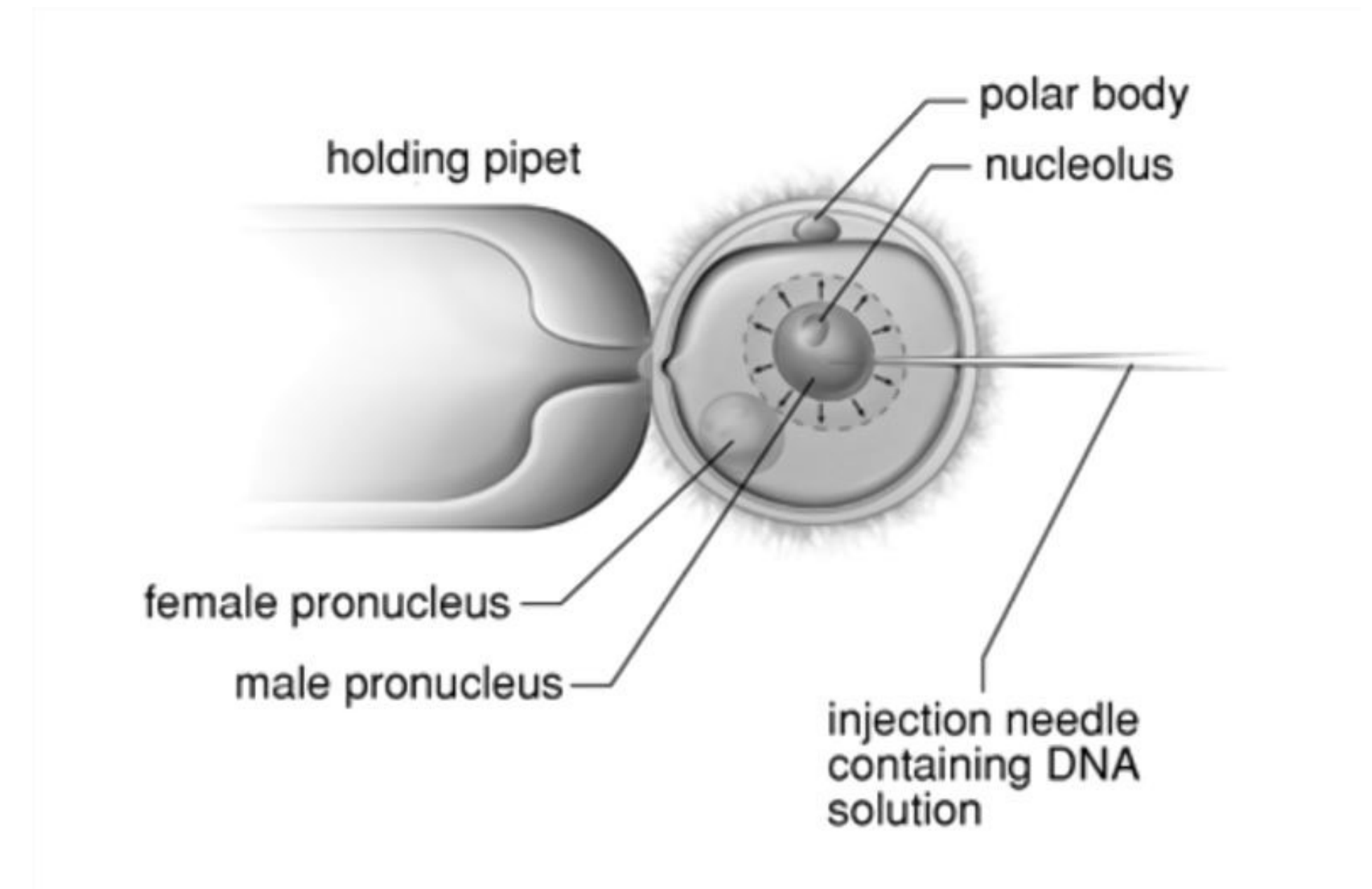
- **Bacterial Artificial Chromosome**
- Artificial circular chromosomes based on E.coli F-plasmids
- Can accommodate larger DNA fragments ranging in size up to 300 kb.
- YACs are similar but grow in Yeast not bacteria. Can accommodate up to 2000 Kb
- DNA fragments have to be introduced by restriction digestion.
- Useful for large genomic DNA fragments, often used as donors for mouse genetic engineering
- Not useful for small constructs



# Transgenic Techniques - mammals

## DNA microinjection

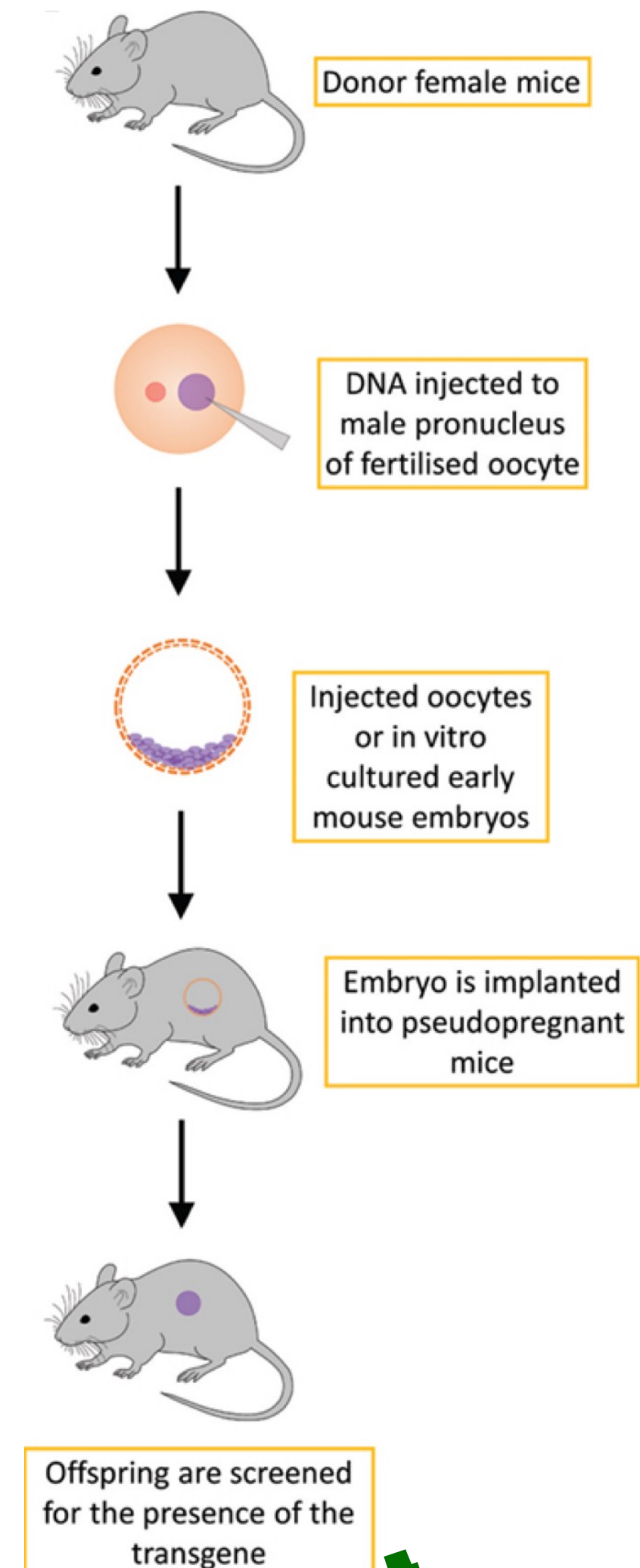
- A plasmid, cosmid or BAC is microinjected
- DNA is introduced into the pronucleus of a developing zygote
- Eggs that survive the injections are transferred into the oviduct of a foster mother.



# Transgenic Techniques - mammals

## DNA microinjection

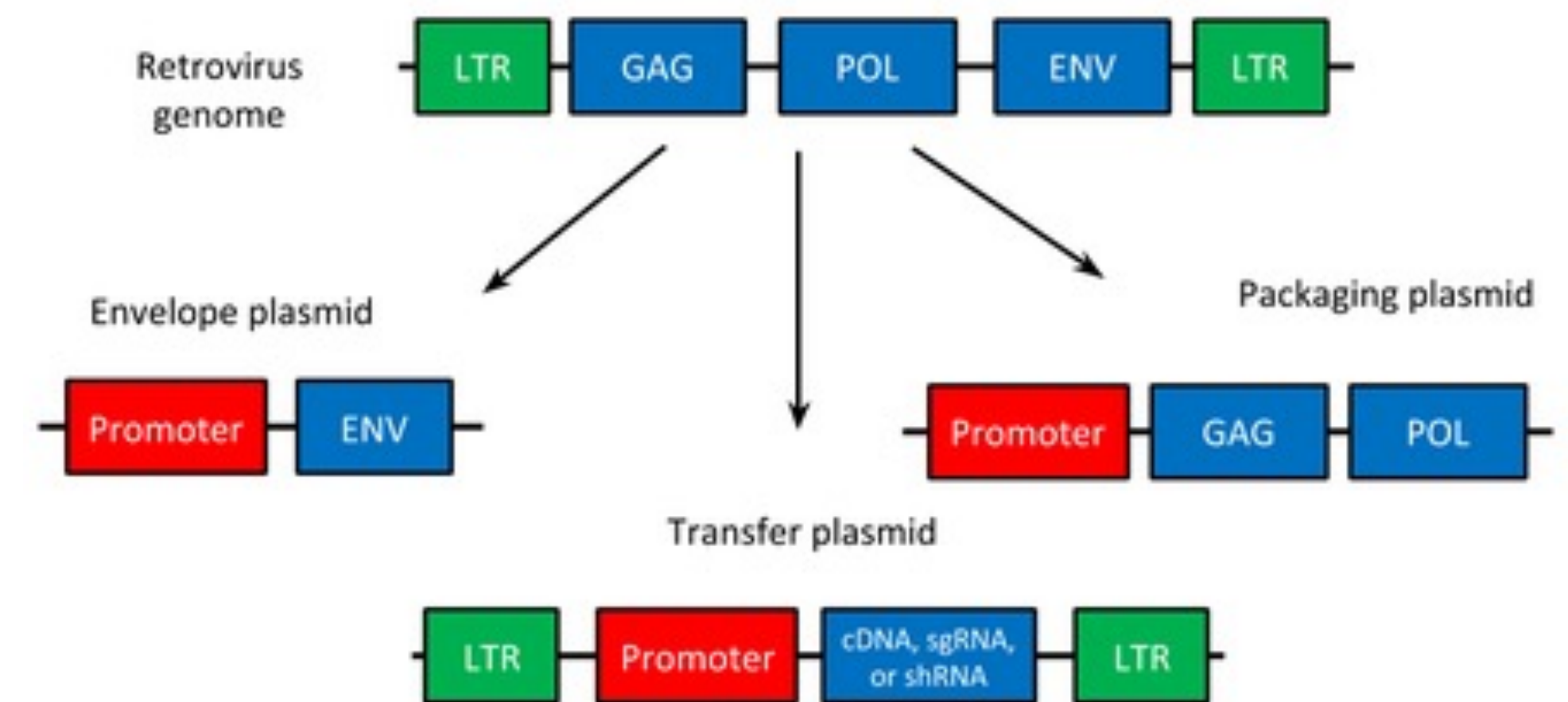
- Widely used
- The amount of DNA delivered per cell is not limited
- Broadly useful across mammalian hosts
- Low success rate
- Mosaic founders
- **Random integration**



# Transgenic Techniques - mammals

## DNA microinjection with retrovirus

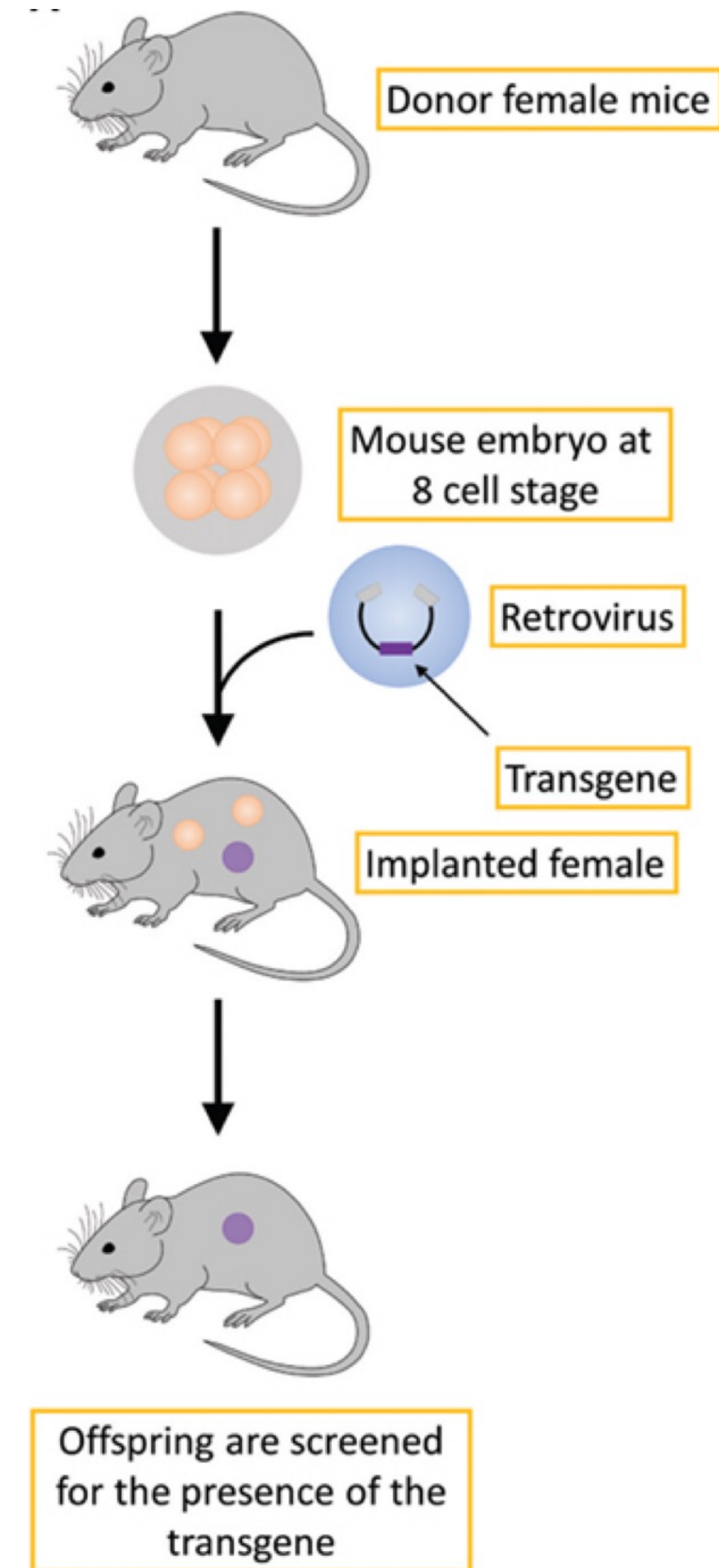
- Commonly use  $\gamma$ -retroviruses (gamma-retroviruses)
- Mostly derived from MoMLV (Moloney Murine Leukemia Virus) or MSCV (Murine Stem Cell Virus) sequences
- Sequences between and including the LTRs is integrated into the host genome upon viral transduction



# Transgenic Techniques - mammals

## DNA microinjection with retrovirus

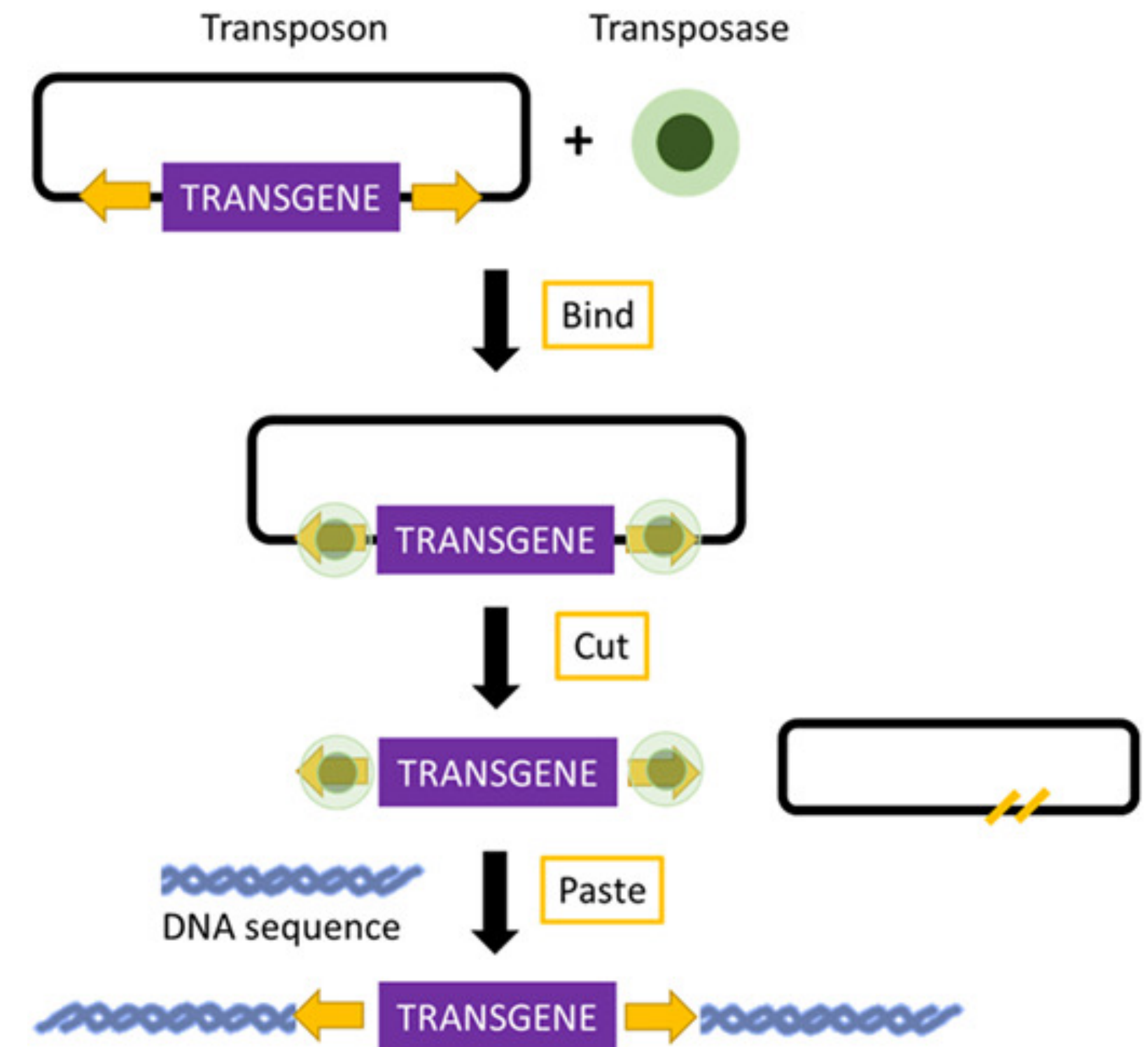
- Virus integration is very efficient
- The amount of DNA delivered per cell is **limited** by virus size max 8.5Kb, but ~3Kb is better
- **Random** integration
- Transgene can be silenced by DNA methylation



# Transgenic Techniques - transposons

## Transposons

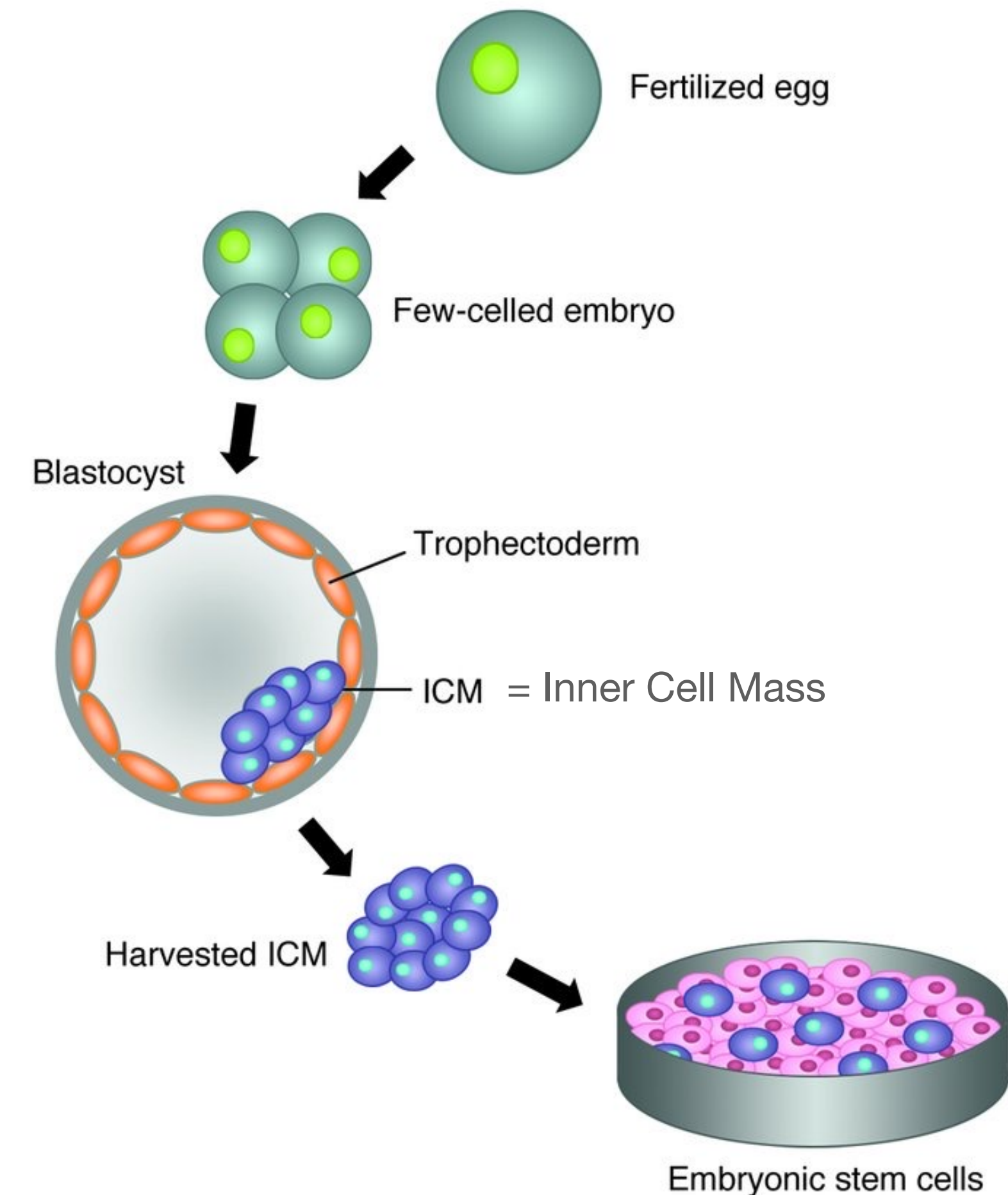
- Transposons, ‘jumping genes’, are genetic elements that can translocate within the genome – Selfish genetic elements
- Transposition process requires sequences at the ends of the transposon and a specific transposase protein
- Can be engineered to replace internal sequences with transgenes
- Have specific sequence preferences e.g. PiggyBac - TTAA
- Random insertion



# Transgenic Techniques - mammals

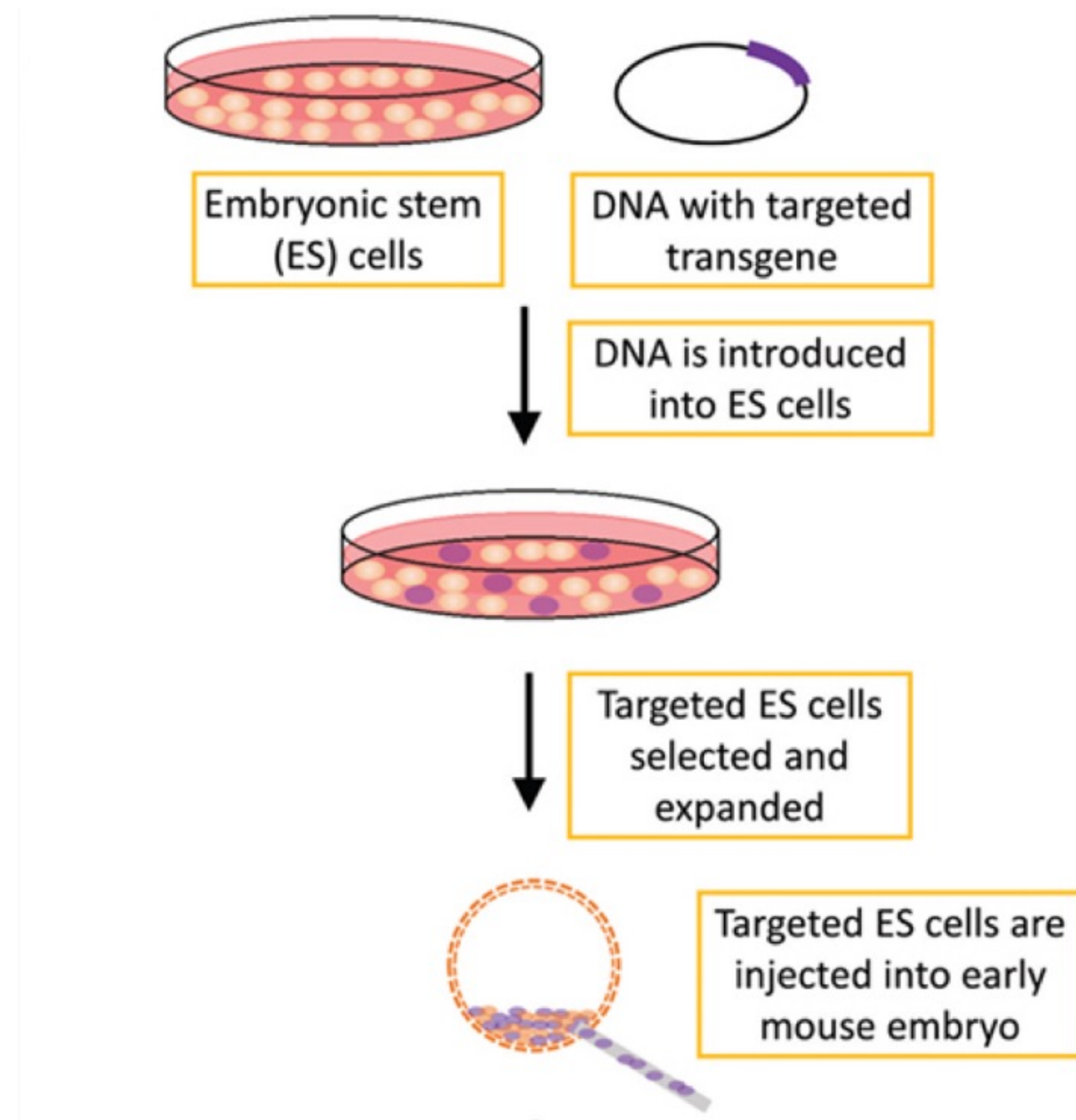
## Embryonic Stem Cells (ES cells)

- ES cells are derived from cells of the early embryos (late blastocyst stage)
- Have the capacity to self-renew indefinitely.
- Pluripotent i.e. can differentiate into all cell types in the body including germ cells



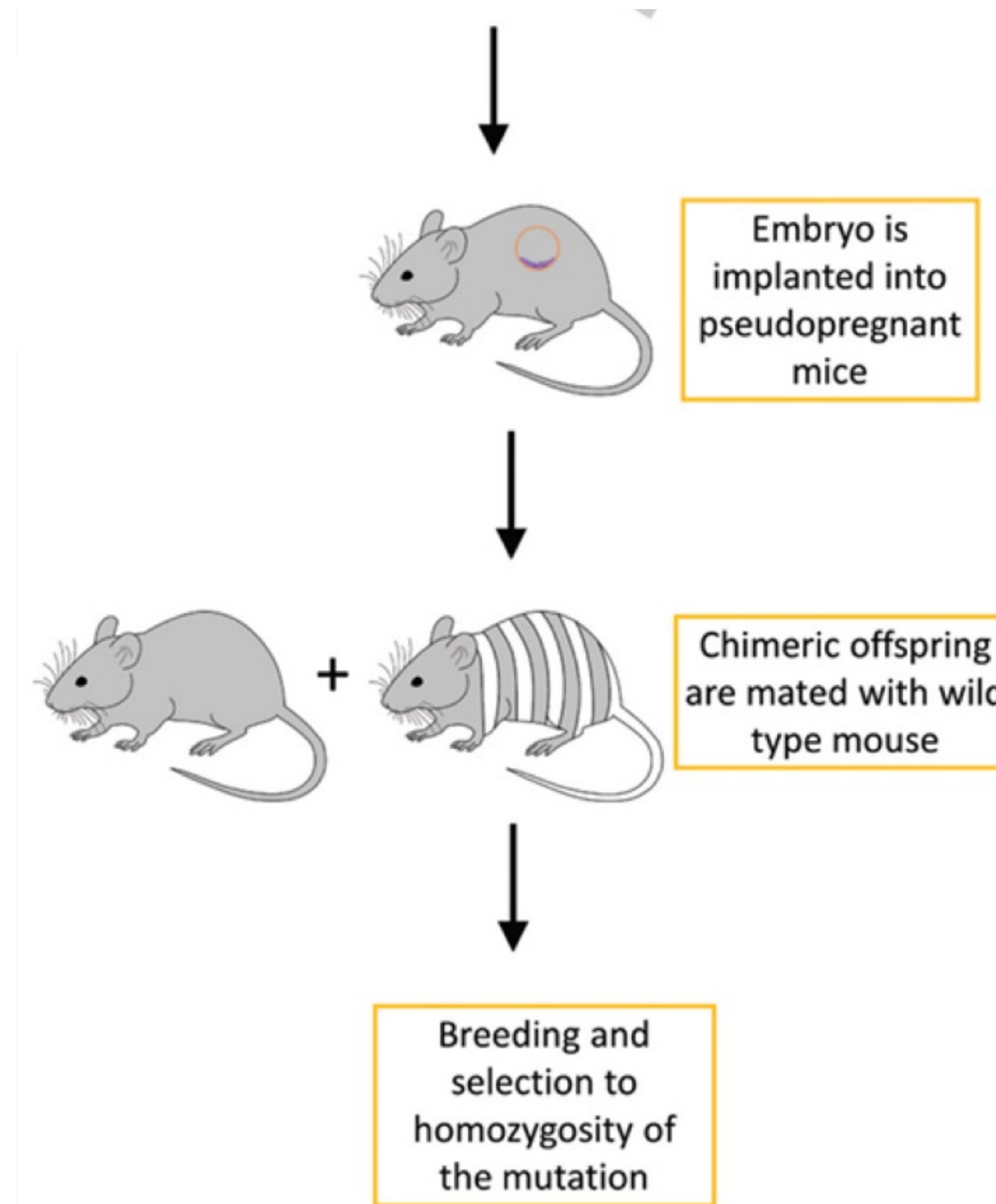
# Transgenic Techniques - mammals

## Introducing transgenes using ES cells



# Transgenic Techniques - mammals

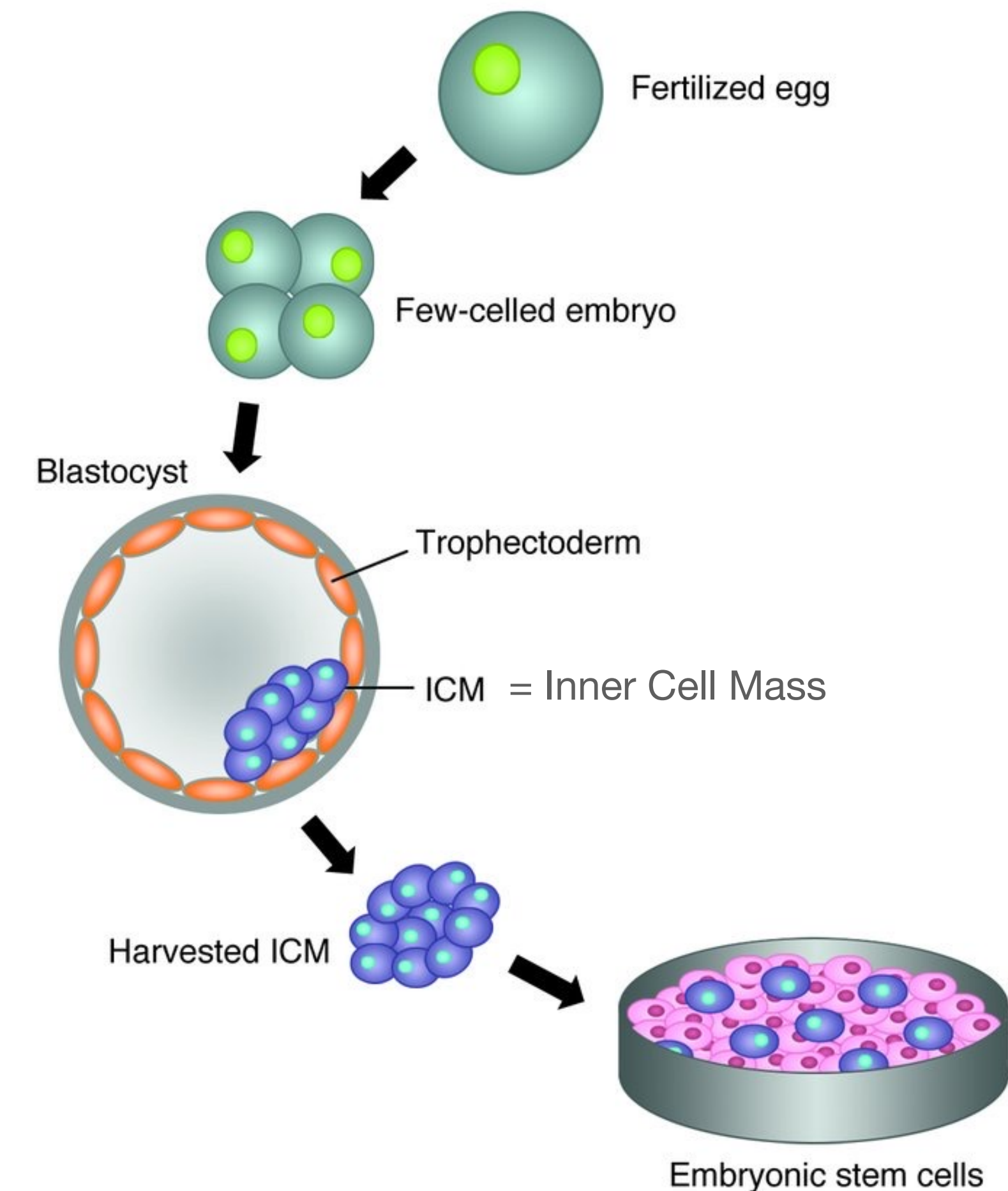
Introducing transgenes using ES cells



# Transgenic Techniques - mammals

## Introducing transgenes using ES cells

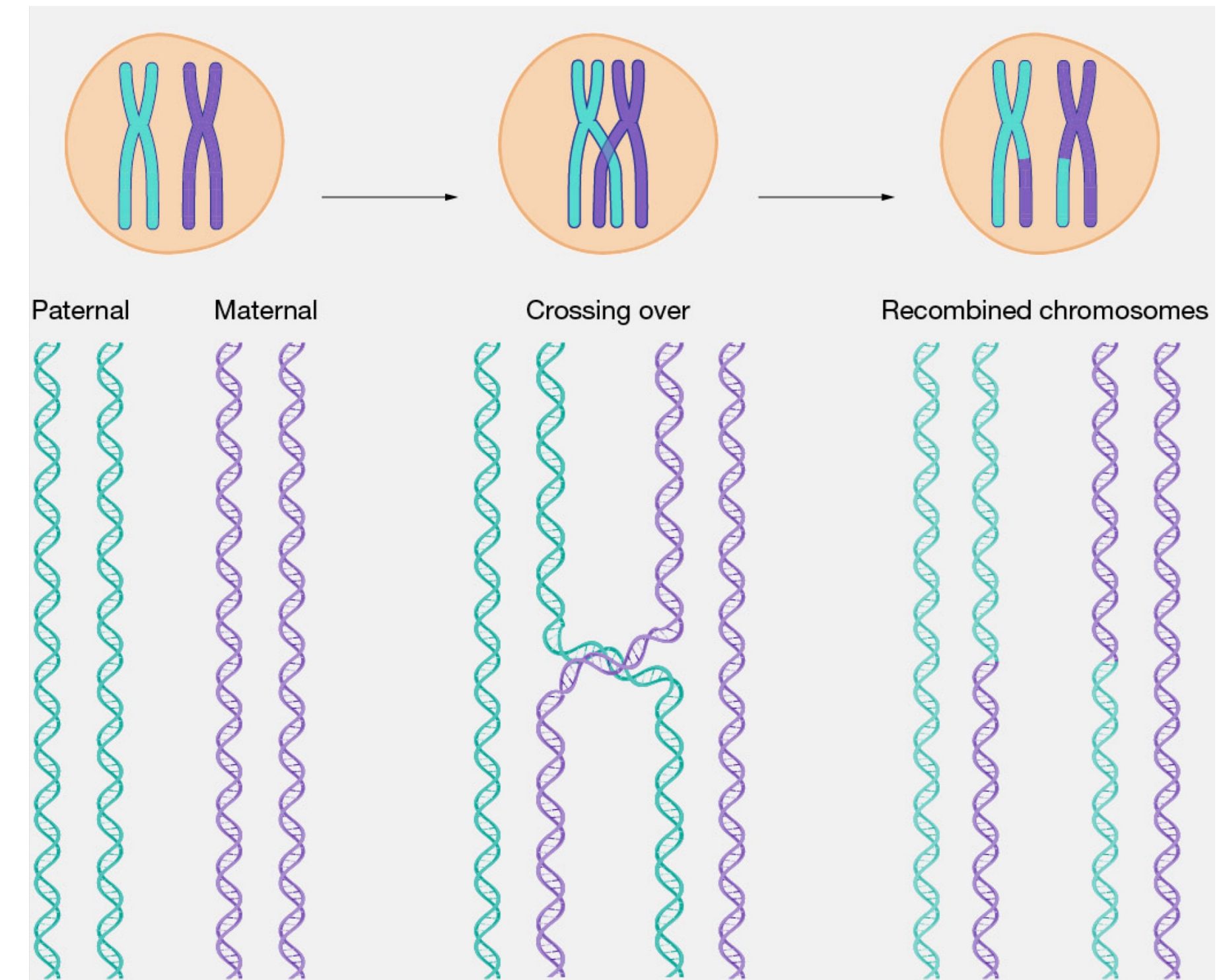
- Efficient through use of cell selectable markers
- Transgene location can be confirmed in ES cells
- Takes longer to have completely transgenic animals.



# Transgenic Techniques - mammals

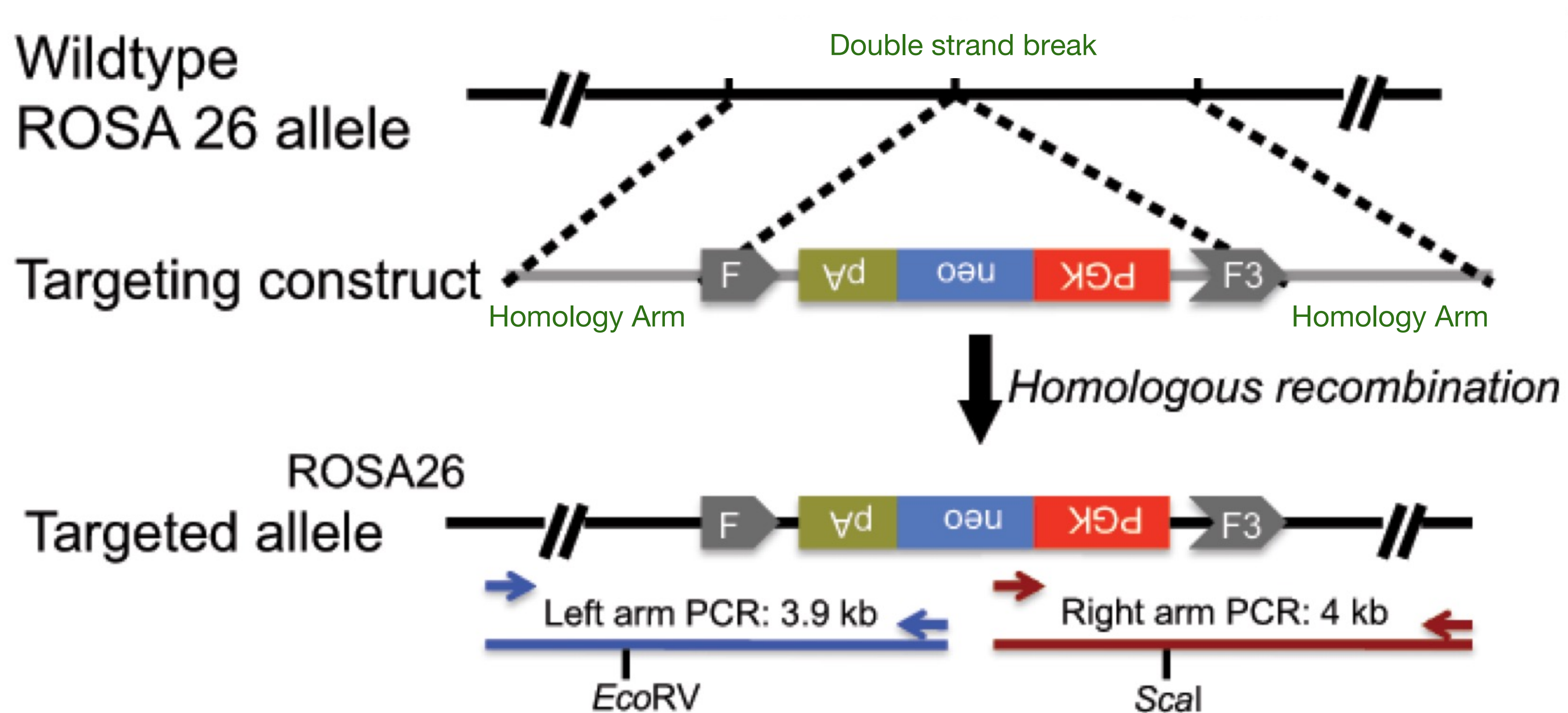
## Targeting transgenes to specific locations

- Homologous recombination is a series of processes that enable the repair of DNA and allow interstrand crosslinks.
- essential to exploit the redundancy of genetic information that exists in the form of sister chromatids or homologous chromosomes
- Very important when both strands of the DNA double helix are compromised (double-strand breaks).
- Used during DNA replication somatic cells and during meiosis.



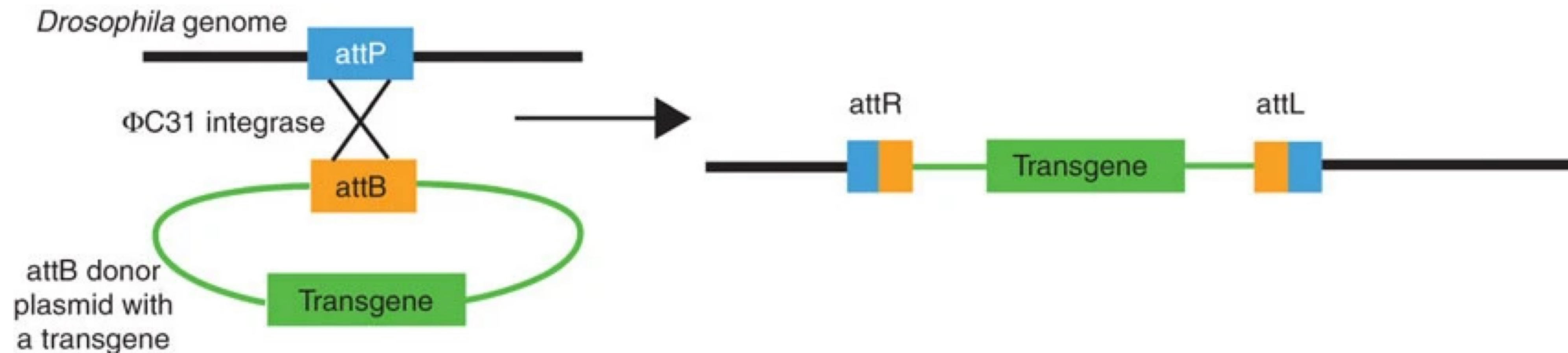
# Transgenic Techniques - mammals

Targeting transgenes to specific locations



# Transgenic Techniques - recombinase

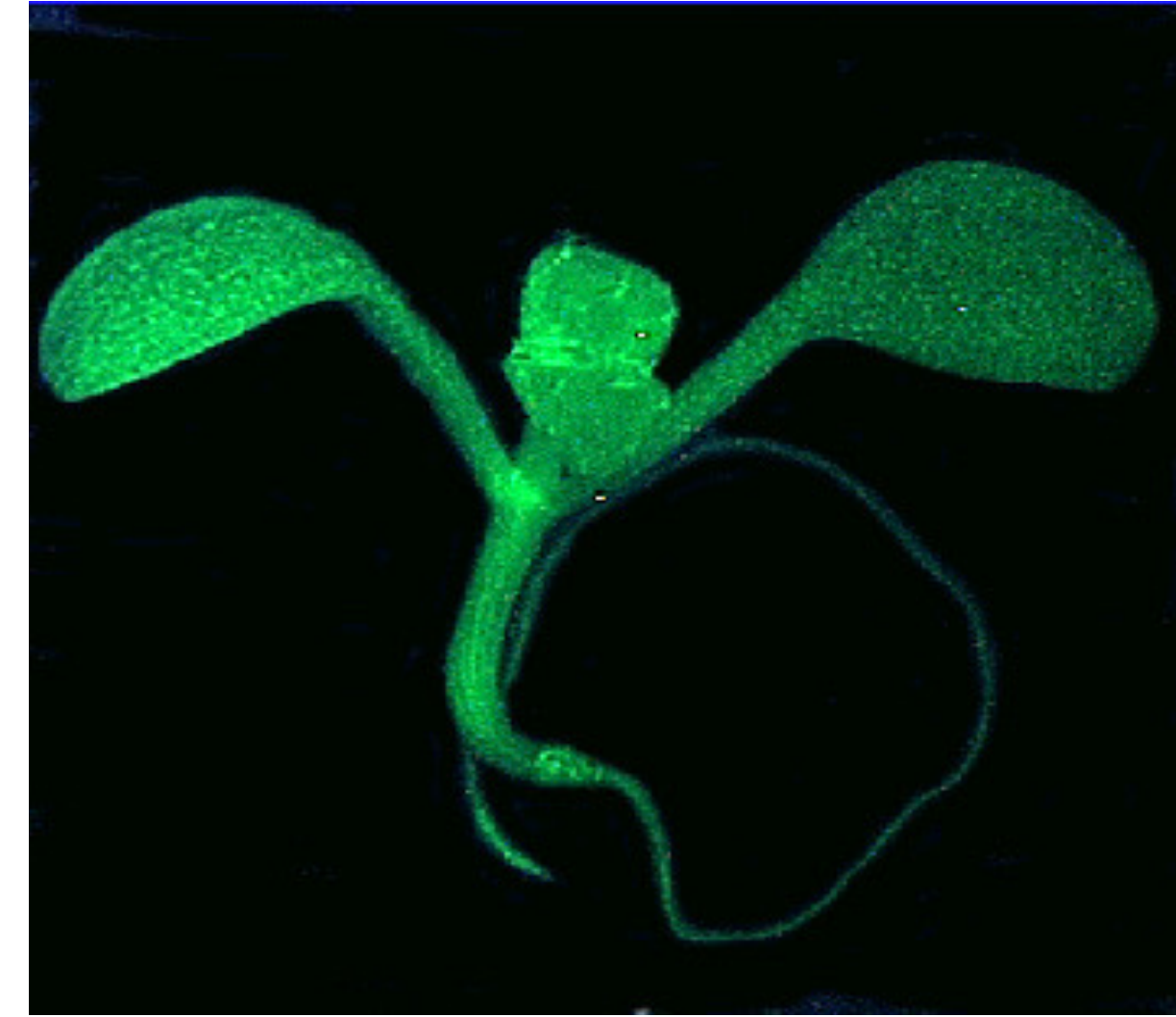
## Drosophila - Targeting transgenes phiC31



- A preplaced (with transposon) attP sequence (attP) acts as the recipient site in the *Drosophila* genome. These sequences are derived from phages.
- An attB plasmid containing both a transgene and donor sequence (attB) is injected together with  $\phi$ C31 integrase mRNA into attP-containing recipient embryos
- This results in the site-specific insertion of the transgene into the attP site.

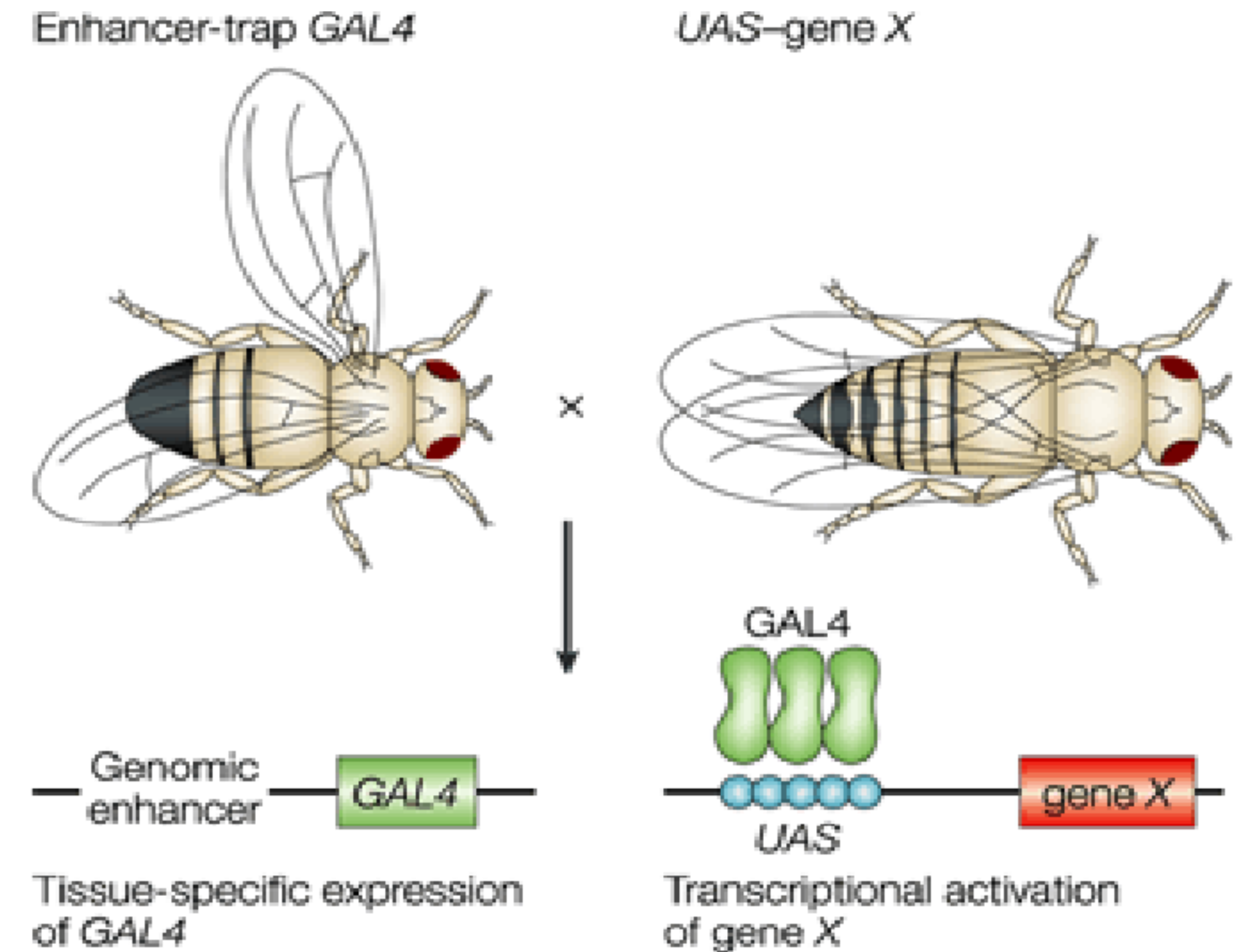
# How do I know my animal is transgenic?

- Molecular confirmation e.g. PCR, commonly used in mice
- Selectable marker e.g. GFP
- Rescue of a mutant phenotype e.g. coat colour, eye colour



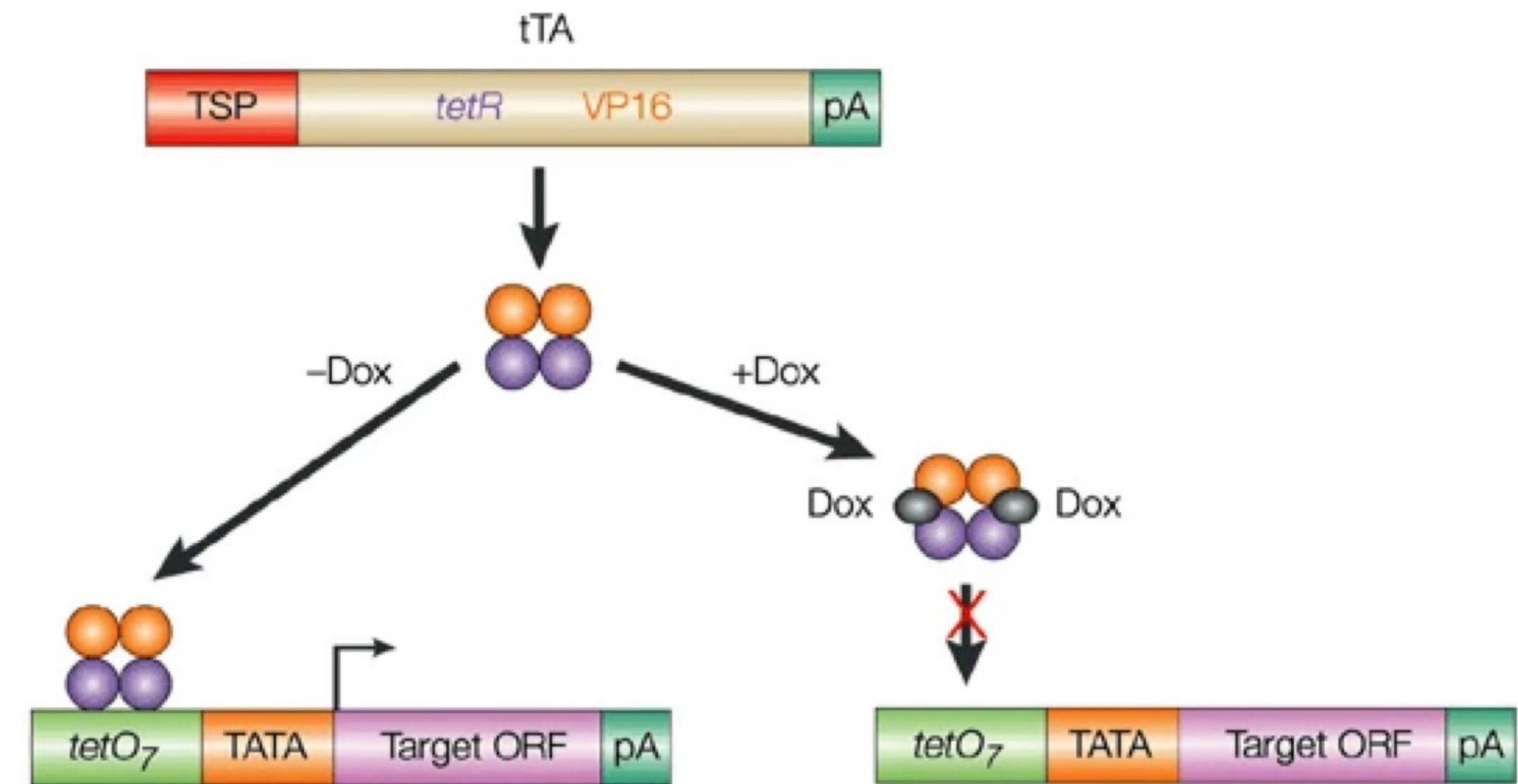
# Controlling transgene expression - space

- Binary gene expression system
- Yeast derived Gal4 transcription factor is expressed under control on tissue specific enhancer sequence
- Transgene has Gal4 binding UAS (upstream activating sequence) before gene to be expressed. Without Gal4 – no expression
- In tissues that express Gal4, gene is expressed. Many UAS regulated genes can be expressed simultaneously.



# Controlling transgene expression - time

- **Tet-Off**
- Tetracycline-controlled transactivator (tTA) of transcription regulates gene expression.
- In the absence of the drug doxycycline (Dox), tTA dimers specifically bind to tetO sequences, activating transcription of the target transgene
- When Dox is provided , tTA undergoes a conformational change and cannot bind tetO sequences.
- Tet-On and other variants available

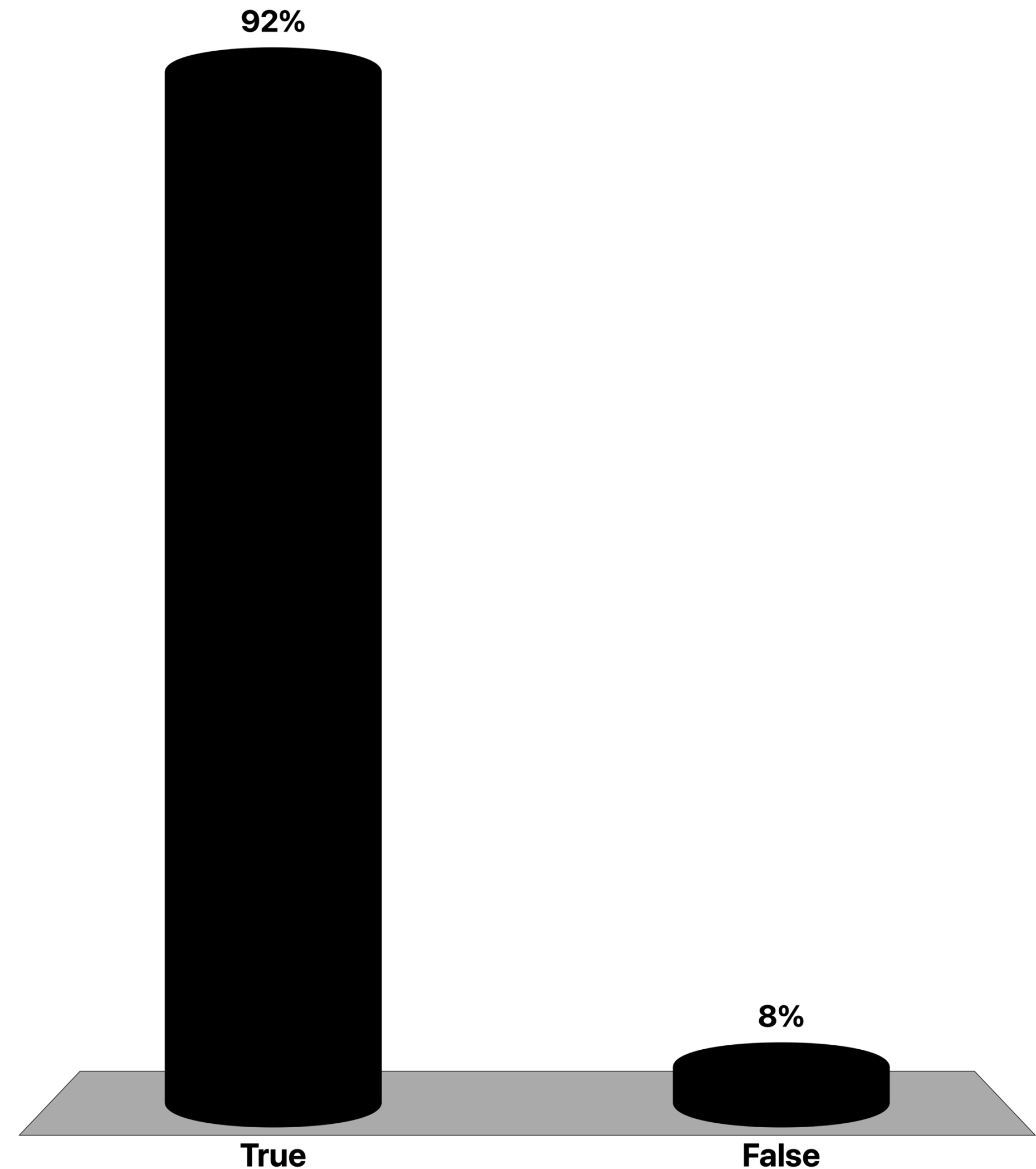




# In Person quiz

# Transgenes can be introduced into humans

- A. True
- B. False



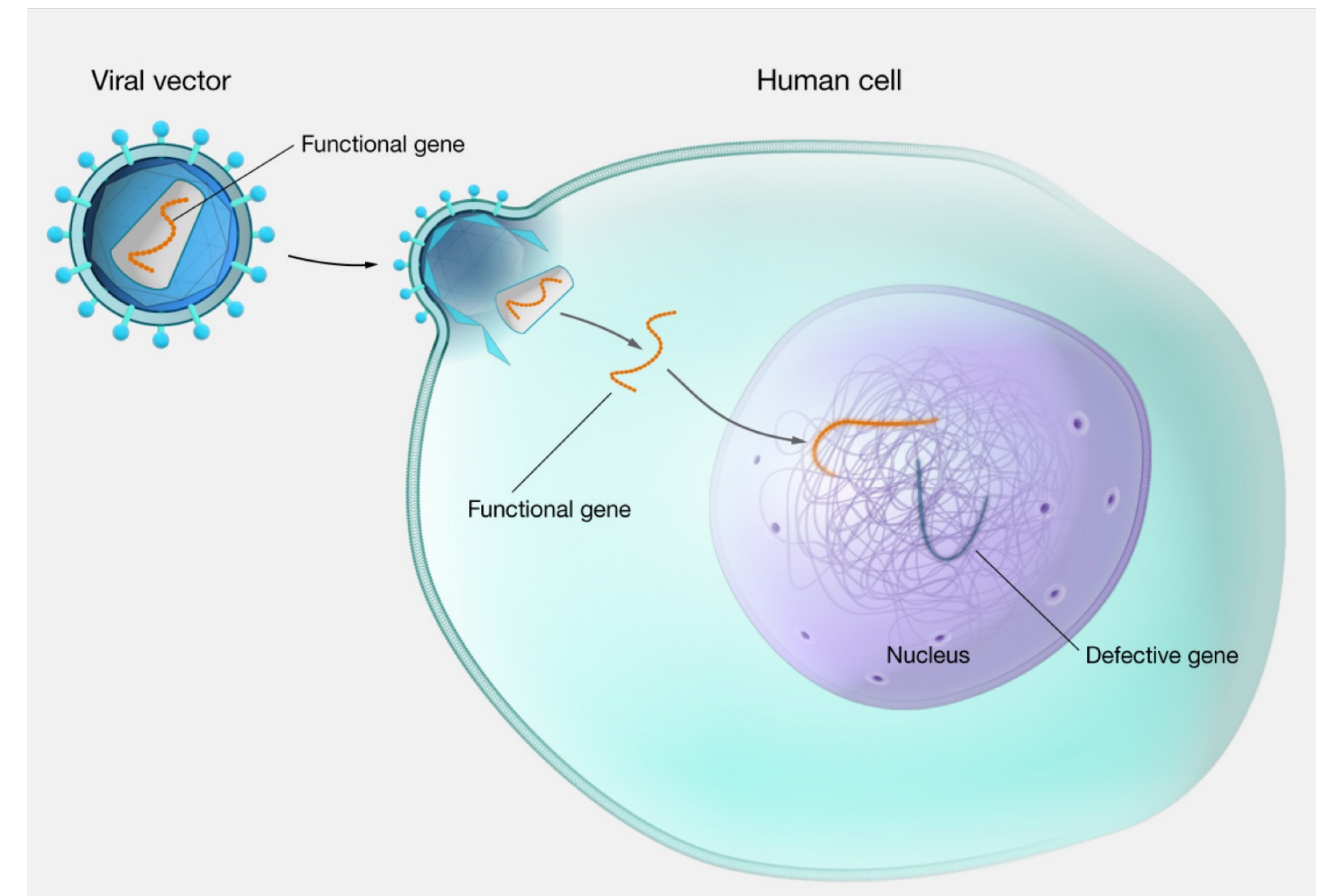


# Gene Therapy

# Gene Therapy

## Treating humans with transgenes

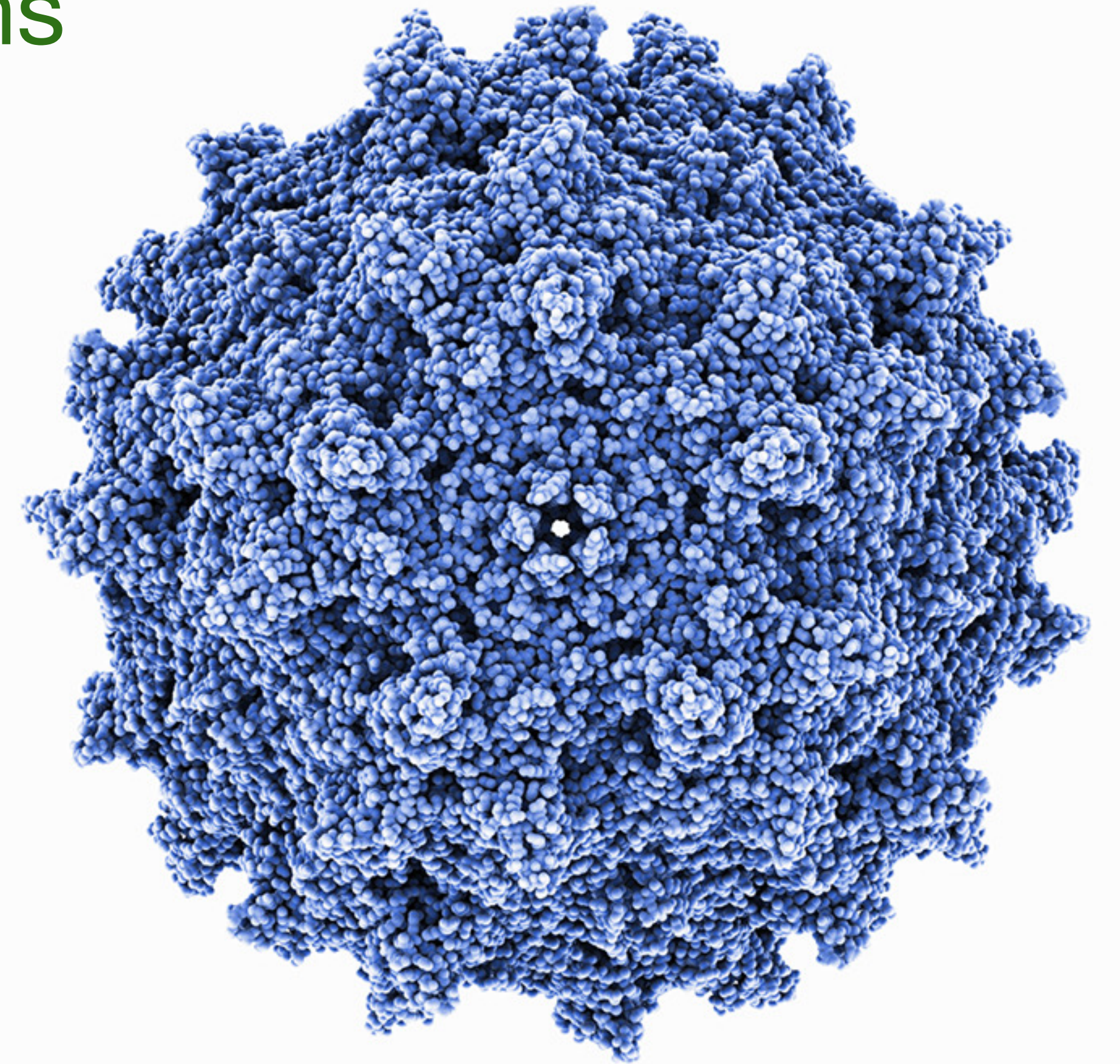
- Gene therapy uses genetic technology to treat, prevent or cure a disease or medical disorder.
- Commonly utilises additional new copies of a gene to compensate for a defective or absent gene in a patient



# AAV

## Targeting transgenes to specific locations

- Adeno-associated viruses (AAV) viruses that infect humans and some other primates.
- Are not thought to cause disease but can elicit a mild immune response.
- Single-stranded DNA genome of 4.8 Kb
- **Does not integrate into genome**



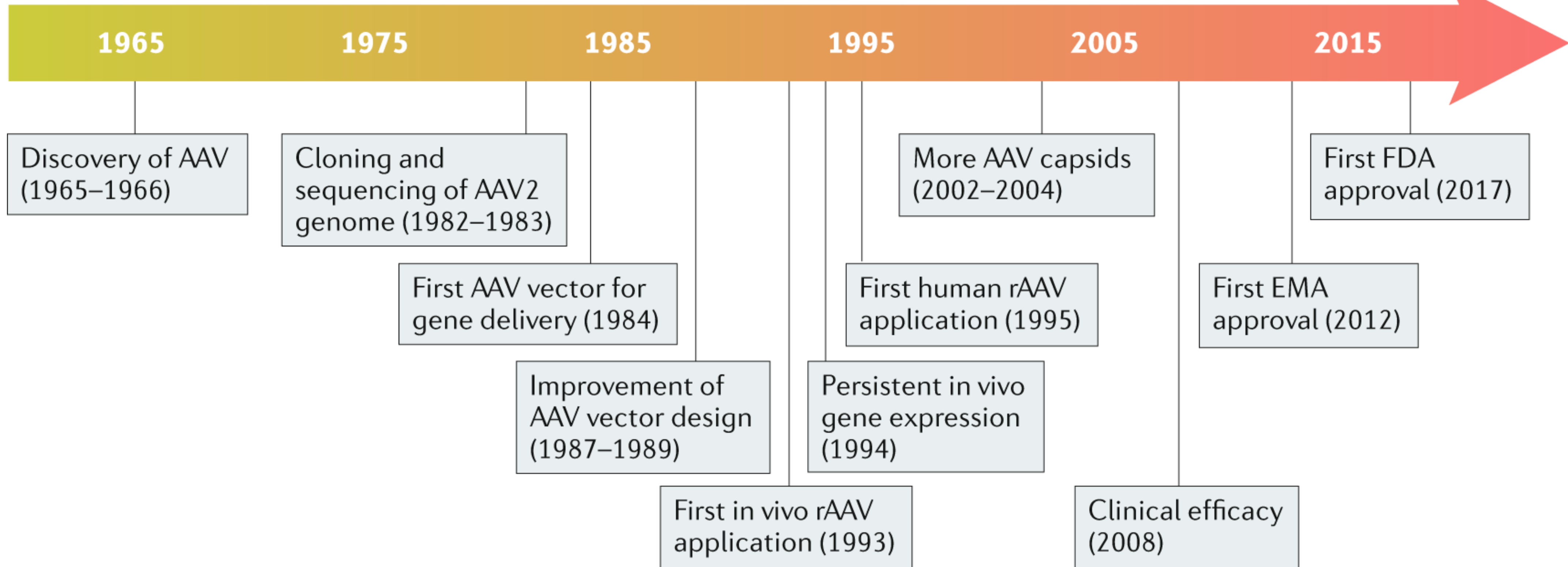
# AAV

Bench to bedside, back to bench, etc.

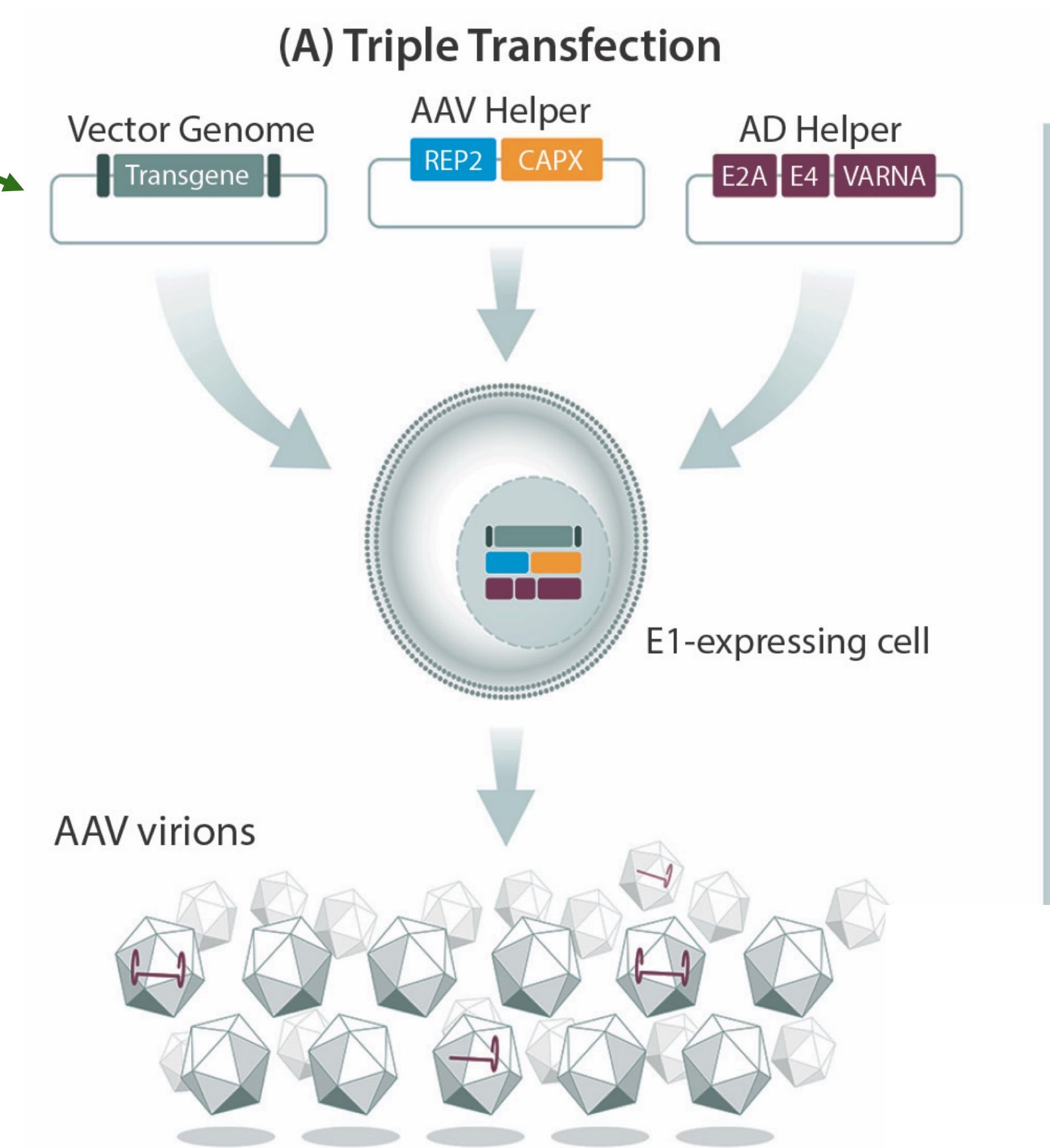
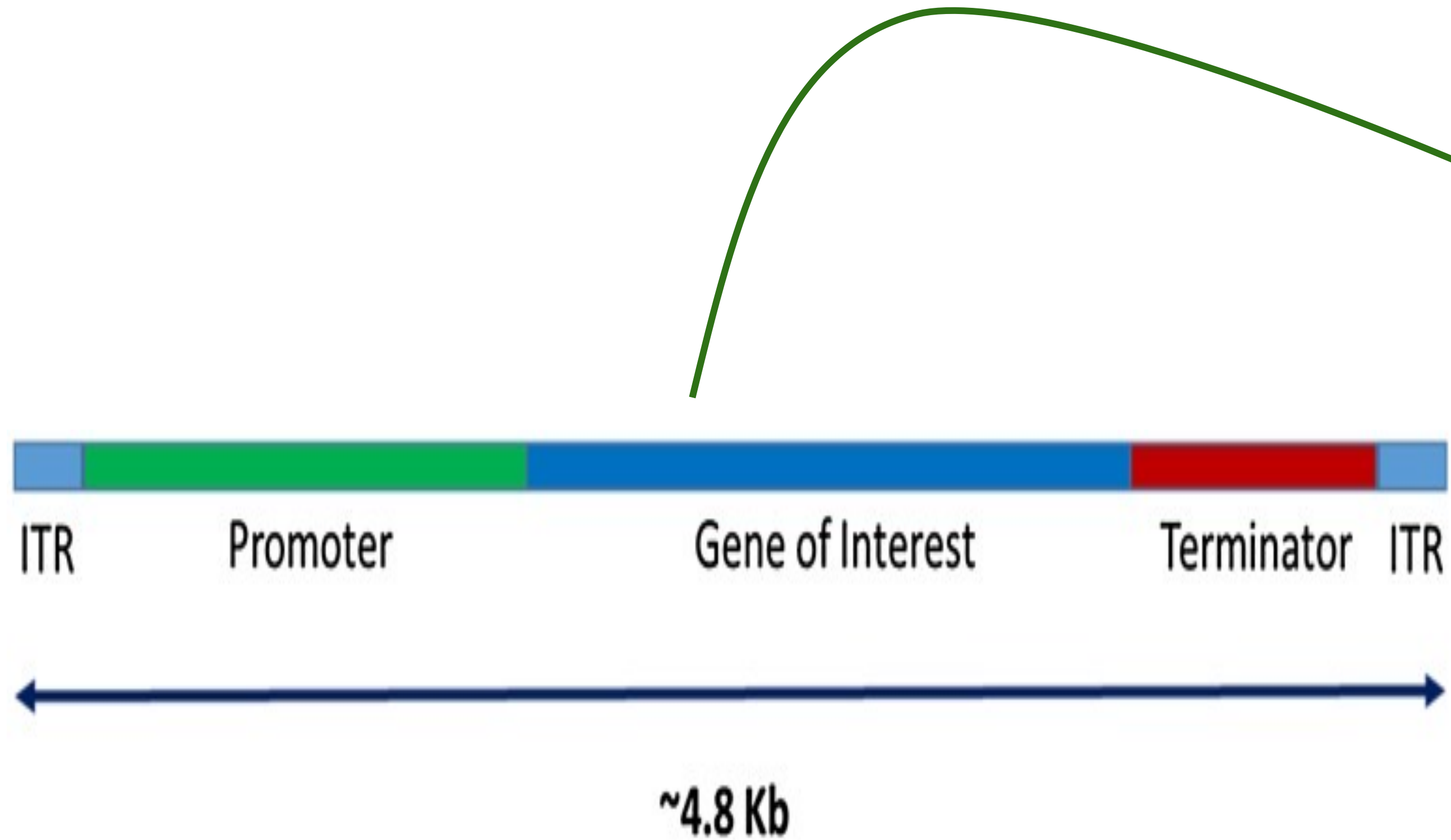
Basic AAV biology

Early gene therapy application

Explosion of clinical trials



# AAV



# Spinal Muscular Atrophy (SMA)



## SMA Type I

Severe form  
Never sit  
Limited life expectancy  
Respiratory failure

Birth Prevalence 60%



## SMA Type II

Intermediate form  
Sitting or standing  
Life expectancy shortened  
Skeletal deformities

Birth Prevalence 27%

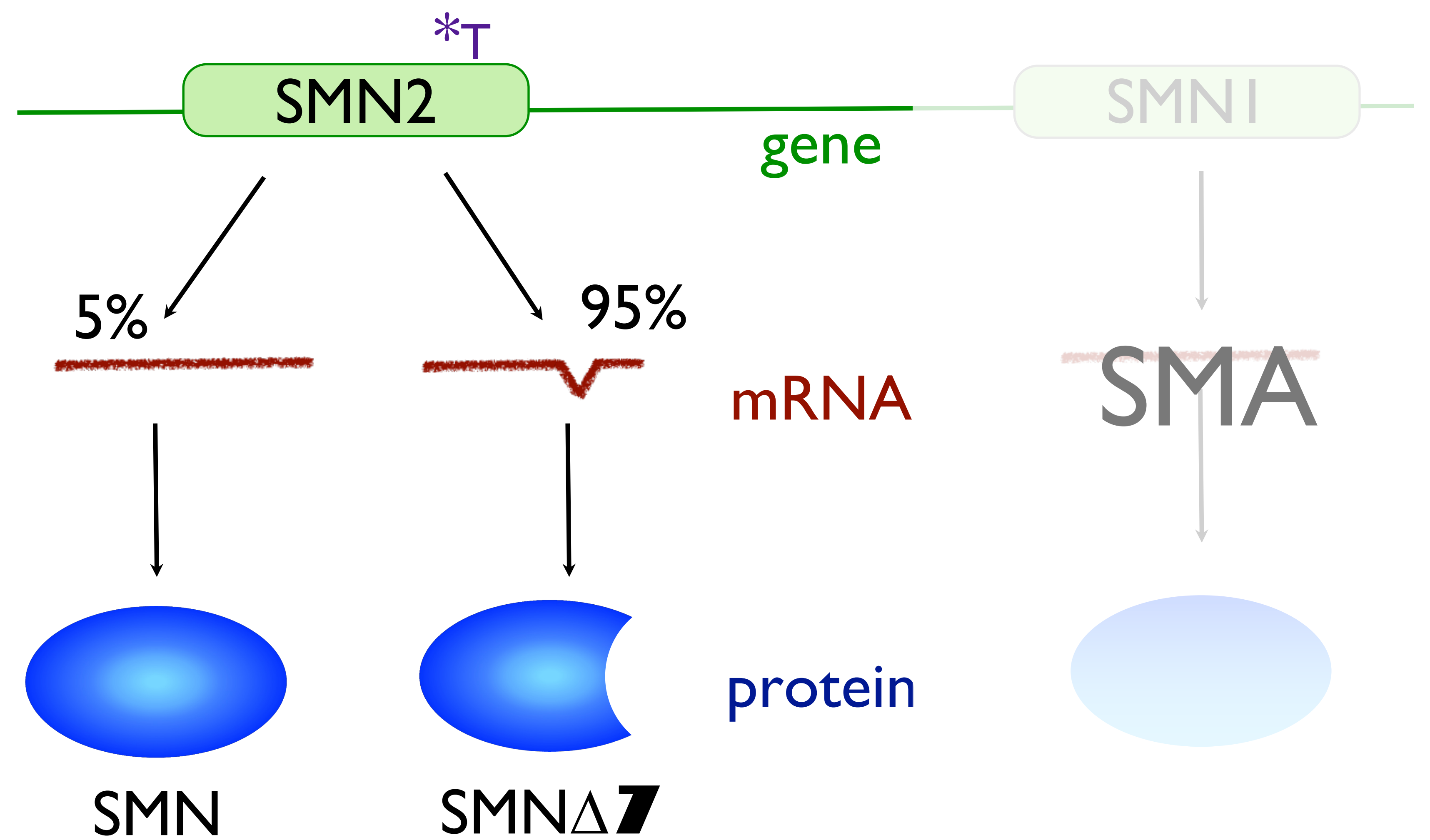


## SMA Type III

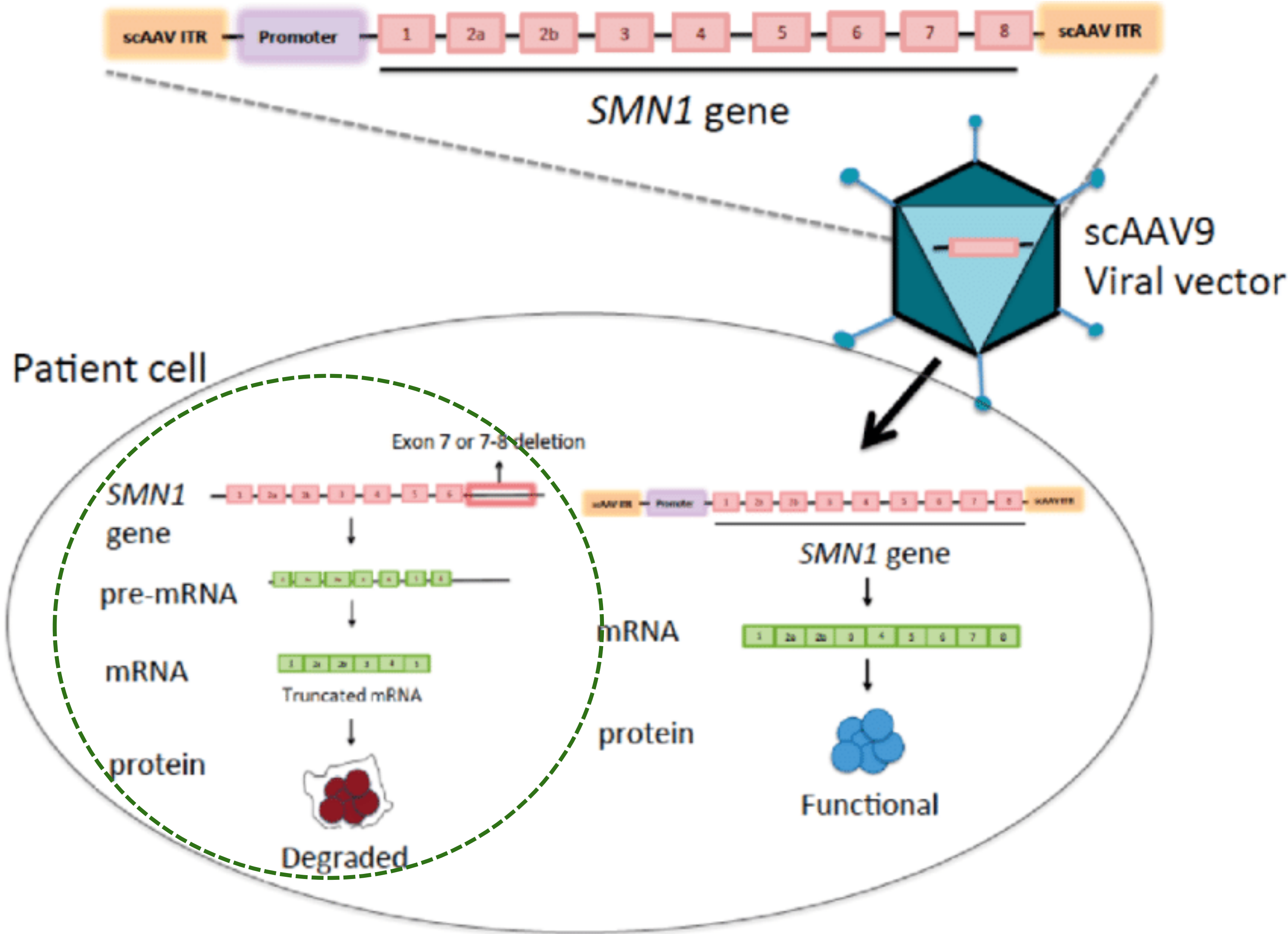
Mild form  
Walkers at some point  
Life expectancy (nearly) normal  
Proximal weakness prominent

Birth Prevalence 12%

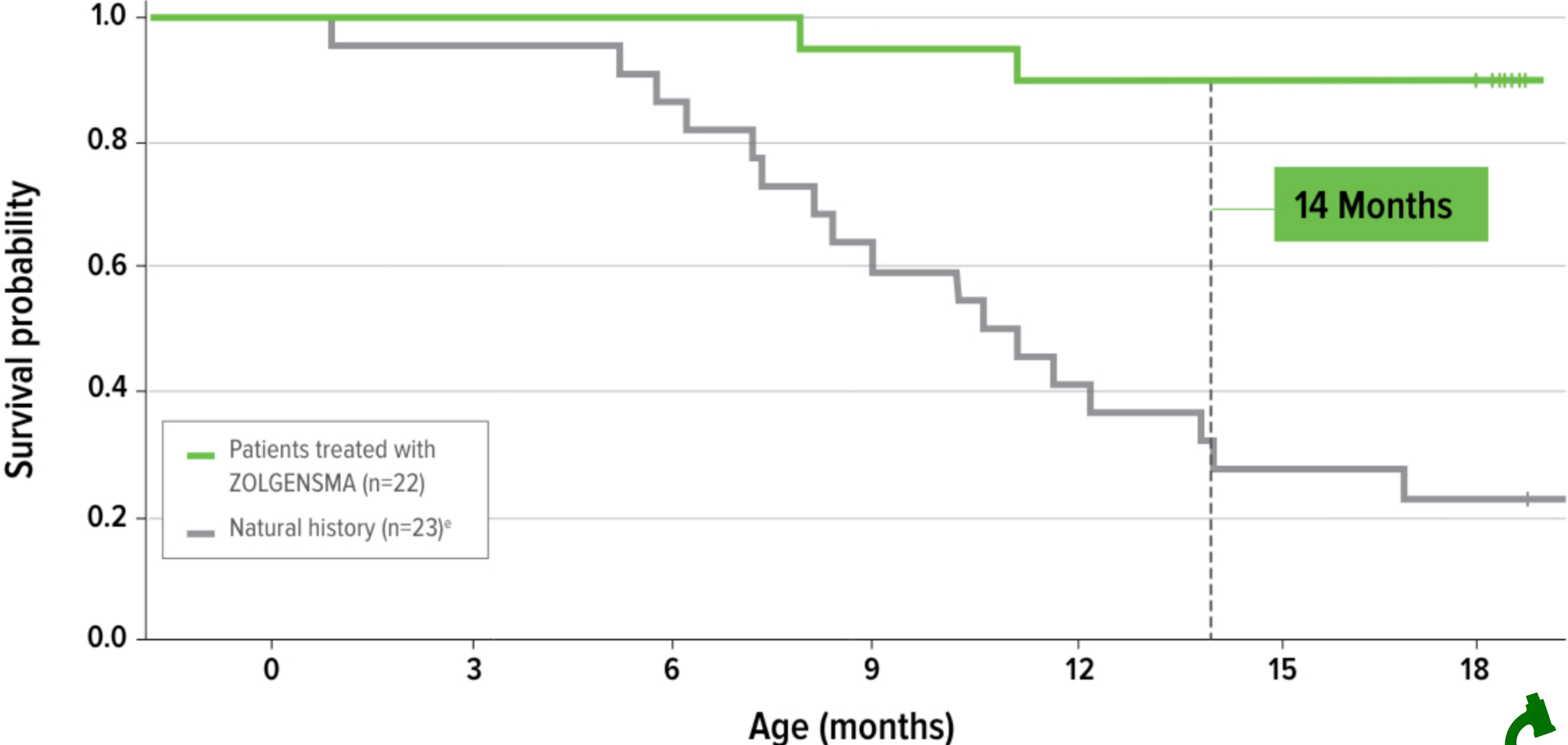
# Reduction of SMN (Survival of Motor Neuron) causes SMA



# Gene Therapy for SMA



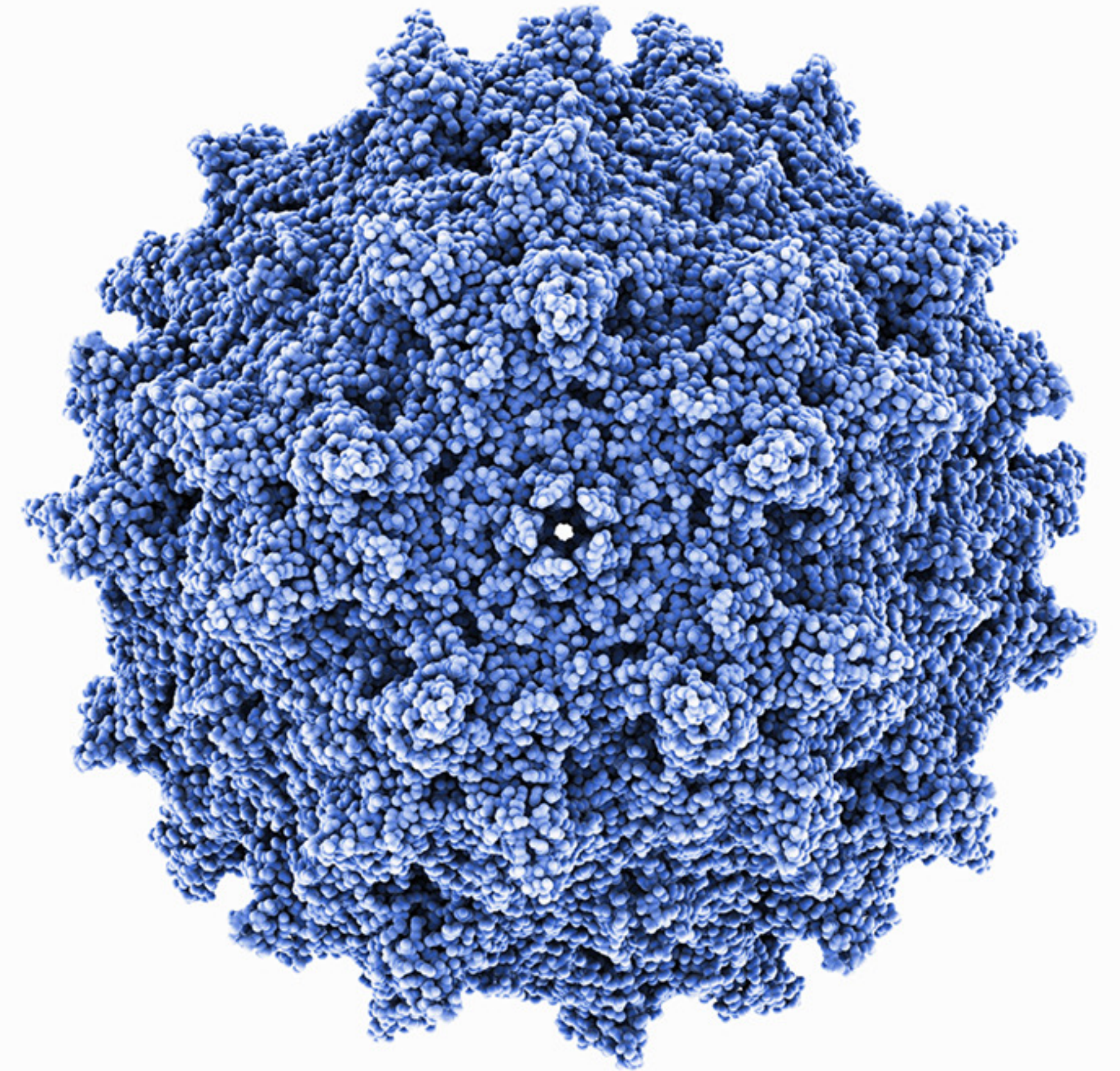
# Gene Therapy for SMA



# AAV gene therapy

## Advantages

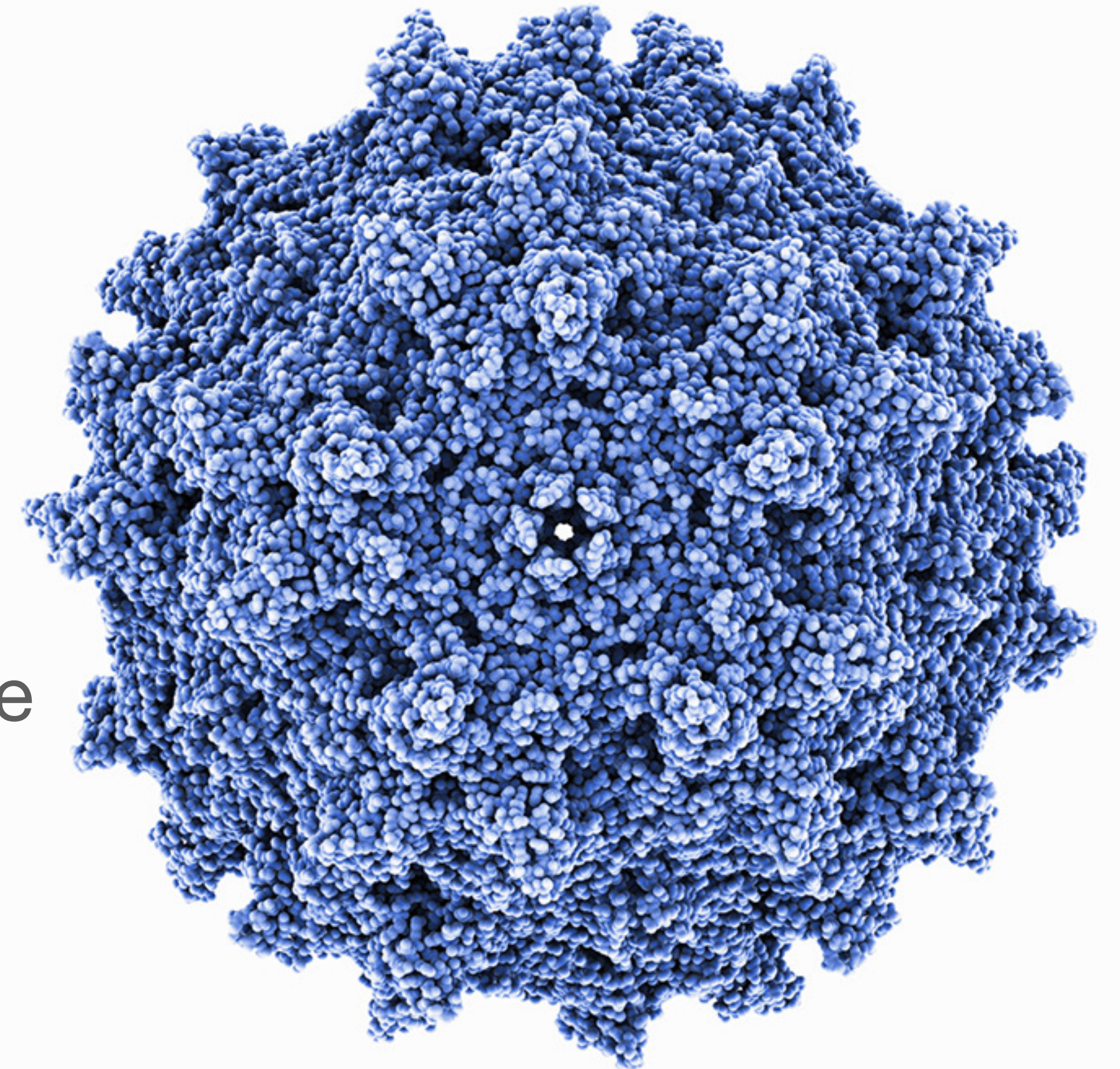
- Single administration
- Does not integrate – could cause mutation.
- Different types of manipulations can be achieved e.g. overexpression or reduction
- Can target cells hard to access with proteins e.g. brain
- May be faster to move from animal model to therapy – i.e. no slow drug development

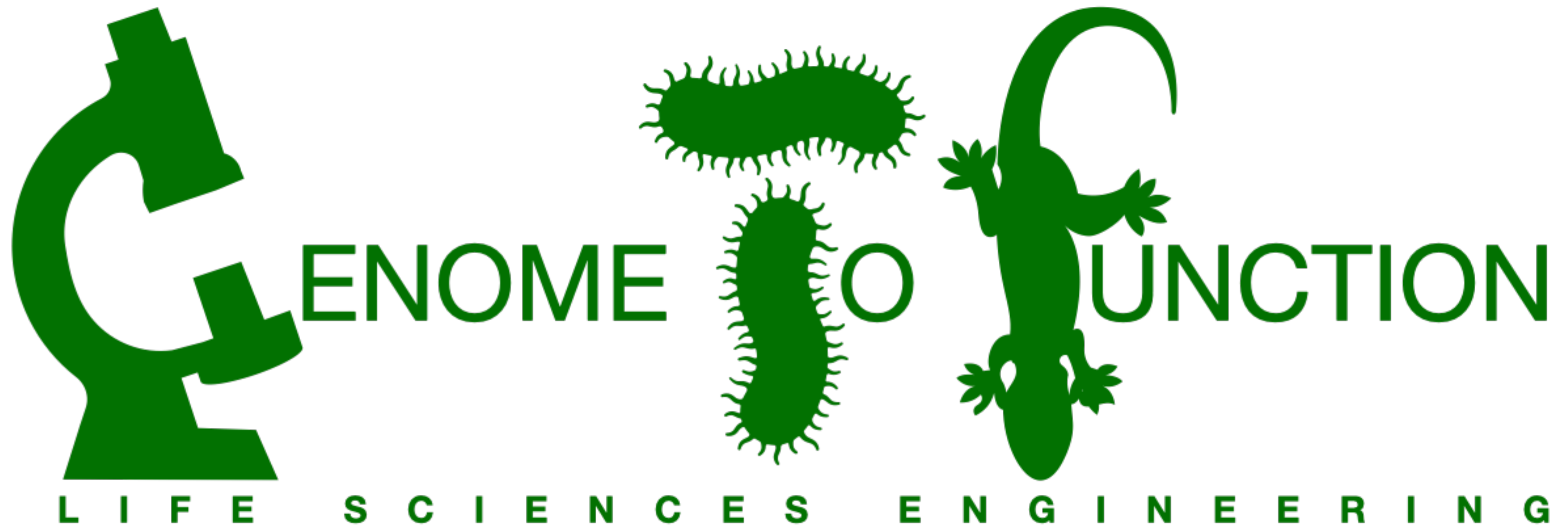


# AAV gene therapy

## Disadvantages

- Small insert size
- Viral vectors have tropism for some cells.
- Hard to target large numbers of cells (e.g. entire brain in adults)
- Expression levels and pattern of gene may not be correct
- Non-integrating virus like AAV will be lost eventually to cell division.
- Expensive – SMA treatment was originally \$2M!





**Thank You & Questions**